

Fig. 1

met ser lys asn thr  
val ser ser ala arg phe arg lys val asp val asp  
glu tyr asp glu asn lys phe val asp glu glu asp  
gly gly asp gly gln ala gly pro asp glu gly glu  
val asp ser cys leu arg gln gly asn met thr ala  
ala leu gln ala ala leu lys asn pro pro ile asn  
thr **arg** ser gln ala val lys asp arg ala gly ser  
ile val leu lys val leu ile ser phe lys ala **gly**  
asp ile glu lys ala val gln ser leu asp **arg** asn  
gly val asp leu leu met lys tyr ile tyr lys gly  
phe glu ser pro ser asp asn ser ser ala **val** leu  
leu gln trp his glu lys ala leu ala ala gly gly  
val gly ser ile val arg val leu thr ala arg lys  
thr val

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Fig. 2A (1/3)

ggctctgtgtg	tgcgtgcgtg	cgagtgagtg	agtgtgtgca	tatttttttt	tctcttttct		60									
ttctctctct	tttttttttt	tttgcaaaga	aacagcagcg	ccgccgcgcg	tccgccgagg		120									
cgctgcgccc	cccggggggg	ggagggcgag	gaggcgggca	gcggcggagg	gaggggagcc		180									
ggggaggggg	gcgccgcgct	gggagggagg	cagcgcgcac	ggtgcagccg	ggccggggcg		240									
gaggc	atg	gcg	ggg	ccc	ccg	gcc	cta	ccc	ccg	ccg	gag	acg	gcg	gcg	gcc	290
Met	Ala	Gly	Pro	Pro	Ala	Leu	Pro	Pro	Pro	Glu	Thr	Ala	Ala	Ala		
1					5					10					15	
g	c	a	c	c	c	c	c	c	c	c	c	c	c	c	c	
Ala	Thr	Thr	Ala	Ala	Ala	Ala	Ala	Ser	Ser	Ser	Ala	Ala	Ser	Pro	His	338
				20					25					30		
t	a	c	a	a	c	a	a	a	c	a	c	c	c	c	a	
Tyr	Gln	Glu	Trp	Ile	Leu	Asp	Thr	Ile	Asp	Ser	Leu	Arg	Ser	Arg	Lys	386
			35					40					45			
g	c	c	c	c	c	c	a	t	c	c	a	t	c	c	c	
Ala	Arg	Pro	Asp	Leu	Glu	Arg	Ile	Cys	Arg	Met	Val	Arg	Arg	Arg	His	434
		50					55					60				
g	c	c	c	c	c	a	c	c	c	c	c	a	a	c	a	
Gly	Pro	Glu	Pro	Glu	Arg	Thr	Arg	Ala	Glu	Leu	Glu	Lys	Leu	Ile	Gln	482
	65					70					75					
c	a	c	c	c	c	c	a	c	a	a	c	a	c	c	c	
Gln	Arg	Ala	Val	Leu	Arg	Val	Ser	Tyr	Lys	Gly	Ser	Ile	Ser	Tyr	Arg	530
	80				85					90					95	
a	a	c	c	c	c	c	c	c	c	c	a	c	c	c	c	
Asn	Ala	Ala	Arg	Val	Gln	Pro	Pro	Arg	Arg	Gly	Ala	Thr	Pro	Pro	Ala	578
				100					105					110		
c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	
Pro	Pro	Arg	Ala	Pro	Arg	Gly	Gly	Pro	Ala	Ala	Ala	Ala	Ala	Pro	Pro	626
			115					120					125			
c	a	c	c	c	c	c	c	c	c	c	c	c	c	c	c	
Pro	Thr	Pro	Ala	Pro	Pro	Pro	Pro	Pro	Pro	Ala	Pro	Val	Ala	Ala	Ala	674
		130					135					140				
g	c	c	c	c	c	c	c	c	c	c	c	c	c	c	a	
Ala	Pro	Ala	Arg	Ala	Pro	Arg	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Ala	Thr	722
	145					150					155					
g	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	
Ala	Pro	Pro	Ser	Pro	Gly	Pro	Ala	Gln	Pro	Gly	Pro	Arg	Ala	Gln	Arg	770
160					165					170					175	
g	c	c	c	c	c	c	c	c	c	c	c	c	c	c	c	
Ala	Ala	Pro	Leu	Ala	Ala	Pro	Pro	Pro	Ala	Pro	Ala	Ala	Pro	Pro	Ala	818
			180					185					190			

Fig. 2A (continued 2/3)

gcg Ala	gcg Ala	ccc Pro	ccg Pro	gcc Ala	ggc Gly	ccg Pro	cgc Arg	cgc Arg	gcc Ala	ccc Pro	ccg Pro	ccc Pro	gcc Ala	gcc Ala	gcc Ala	866
			195				200						205			
gtc Val	gcc Ala	gcc Ala	cgg Arg	gag Glu	tcg Ser	ccg Pro	ctg Leu	ccg Pro	ccg Pro	ccg Pro	cca Pro	cag Gln	ccg Pro	ccg Pro	gcg Ala	914
			210				215						220			
ccg Pro	cca Pro	cag Gln	cag Gln	cag Gln	cag Gln	cag Gln	ccg Pro	ccg Pro	ccg Pro	cca Pro	ccg Pro	ccg Pro	ccg Pro	cag Gln	cag Gln	962
			225				230						235			
cca Pro	cag Gln	ccg Pro	ccg Pro	ccg Pro	gag Glu	ggg Gly	ggc Gly	gcg Ala	gcg Ala	cgg Arg	gcc Ala	ggc Gly	ggc Gly	ccg Pro	gcg Ala	1010
			240				245						250			255
cgg Arg	ccc Pro	gtg Val	agc Ser	ctg Leu	cgg Arg	gaa Glu	gtc Val	gtg Val	cgc Arg	tac Tyr	ctc Leu	ggg Gly	ggt Gly	agc Ser	agc Ser	1058
			260							265						270
ggc Gly	gct Ala	ggc Gly	ggc Gly	cgc Arg	ctg Leu	acc Thr	cgc Arg	ggc Gly	cgc Arg	gtg Val	cag Gln	ggt Gly	ctg Leu	ctg Leu	gaa Glu	1106
			275							280						285
gag Glu	gag Glu	gcg Ala	gcg Ala	gcg Ala	cgg Arg	ggc Gly	cgc Arg	ctg Leu	gag Glu	cgc Arg	acc Thr	cgt Arg	ctc Leu	gga Gly	gcg Ala	1154
			290							295						300
ctt Leu	gcg Ala	ctg Leu	ccc Pro	cgc Arg	ggg Gly	gac Asp	agg Arg	ccc Pro	gga Gly	cgg Arg	gcg Ala	cca Pro	ccg Pro	gcc Ala	gcc Ala	1202
			305							310						315
agc Ser	gcc Ala	cgc Arg	gcg Ala	gcg Ala	cgg Arg	aac Asn	aag Lys	aga Arg	gct Ala	ggc Gly	gag Glu	gag Glu	cga Arg	gtg Val	ctt Leu	1250
			320				325						330			335
gaa Glu	aag Lys	gag Glu	gag Glu	gag Glu	gag Glu	gag Glu	gag Glu	gag Glu	gaa Glu	gac Asp	gac Asp	gag Glu	gac Asp	gac Asp	gac Asp	1298
			340							345						350
gac Asp	gac Asp	gtc Val	gtg Val	tcc Ser	gag Glu	ggc Gly	tcg Ser	gag Glu	gtg Val	ccc Pro	gag Glu	agc Ser	gat Asp	cgt Arg	ccc Pro	1346
			355							360						365
gcg Ala	ggt Gly	gcg Ala	cag Gln	cat His	cac His	cag Gln	ctg Leu	aat Asn	ggc Gly	ggc Gly	gag Glu	cgc Arg	ggc Gly	ccg Pro	cag Gln	1394
			370							375						380
acc Thr	gcc Ala	aag Lys	gag Glu	cgg Arg	gcc Ala	aag Lys	gag Glu	tgg Trp	tcg Ser	ctg Leu	tgt Cys	ggc Gly	ccc Pro	cac His	cct Pro	1442
			385				390						395			
ggc Gly	cag Gln	gag Glu	gaa Glu	ggg Gly	cgg Arg	ggg Gly	ccg Pro	gcc Ala	gcg Ala	ggc Gly	agt Ser	ggc Gly	acc Thr	cgc Arg	cag Gln	1490
			400				405						410			415

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AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS

Fig. 2A (continued 3/3)

gtg ttc tcc atg gcg gcc ttg agt aag gag ggg gga tca gcc tct tcg	1538
Val Phe Ser Met Ala Ala Leu Ser Lys Glu Gly Gly Ser Ala Ser Ser	
420 425 430	
acc acc ggg cct gac tcc ccg tcc ccg gtg cct ttg ccc ccc ggg aag	1586
Thr Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro Pro Gly Lys	
435 440 445	
cca gcc ctc cca gga gcc gat ggg acc ccc ttt ggc tgc cct gcc ggg	1634
Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys Pro Ala Gly	
450 455 460	
cgc aaa gag aag ccg gca gac ccc gtg gag tgg aca gtc atg gac gtc	1682
Arg Lys Glu Lys Pro Ala Asp Pro Val Glu Trp Thr Val Met Asp Val	
465 470 475	
gtg gag tac ttc acc gag gcg ggc ttc cct gag caa gcc acg gct ttc	1730
Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala Thr Ala Phe	
480 485 490 495	
cag gag cag gag atc gac ggc aag tcc ctg ctg ctc atg cag cgc acc	1778
Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met Gln Arg Thr	
500 505 510	
gat gtc ctc acc ggc ctg tcc atc cgc ctg ggg cca gcg ttg aaa atc	1826
Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala Leu Lys Ile	
515 520 525	
tat gag cac cat atc aag gtg ctg cag cag ggt cac ttc gag gac gat	1874
Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe Glu Asp Asp	
530 535 540	
gac ccg gaa ggc ttc ctg gga t gagcacagag ccgcccgcgc ccttggtcccc	1926
Asp Pro Glu Gly Phe Leu Gly	
545 550	
acccccaccc cgccctggacc cattcctgcc tccatgtcac ccaaggtgtc ccagaggcca	1986
ggagctggac tgggcaggcg aggggtgcgg acctaccctg attctggtag ggggcggggc	2046
cttgcctgtgc tcattgctac cccccaccc cgtgtgtgtc tctgcacctg cccccagcac	2106
acccctcccg gagcctggat gtcgcctggg actctggcct gctcattttg cccccagatc	2166
agccccctcc ctccctcctg tcccaggaca ttttttaaaa gaaaaaaagg aaaaaaaaaa	2226
attggggagg gggctgggaa ggtgccccaa gatcctcctc ggcccaacca ggtgtttatt	2286
cctatatata tatatatatg ttttgttctg cctgtttttc gtttttttgt gcgtggcctt	2346
tcttccctcc caccaccact catggcccca gccctgctcg ccctgtcggc gggagcagct	2406
gggaatggga ggagggtggg accttgggtc tgtctccac cctctctccc gttggttctg	2466
ttgtogctcc agctggctgt attgcttttt aatattgcac cgaagggttg tttttttttt	2526
tttaaataaa attttaaaaa aaggaaaaaa aaaaa	2561

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fig. 2 B

asp cys arg ser ser ser asn asn arg Xaa pro lys  
gly gly ala ala arg ala gly gly pro ala arg pro  
val ser leu arg glu val val arg tyr leu gly gly  
ser ser gly ala gly gly arg leu thr arg gly arg  
val gln gly leu leu glu glu glu ala ala ala arg  
gly arg leu glu arg thr arg leu gly ala leu ala  
leu pro arg gly asp arg pro gly arg ala pro pro  
ala ala ser ala arg ala ala arg asn lys arg ala  
gly glu glu arg val leu glu lys glu glu glu glu  
**glu glu glu** glu asp **asp glu asp asp asp asp**  
**val** val ser glu gly ser glu val pro glu ser asp  
arg pro ala gly ala gln his his gln leu asn **gly**  
gly glu arg gly pro gln **thr** ala lys glu arg **ala**  
lys glu trp **ser leu** cys gly pro his **pro** gly gln  
**glu** glu gly arg gly pro ala **ala** gly ser gly thr  
arg gln val phe ser met ala ala **leu ser** lys glu  
gly gly **ser** ala ser **ser thr** thr gly pro asp ser  
pro ser pro val pro leu pro pro gly lys pro ala  
leu pro gly ala asp gly thr pro phe gly cys pro  
**ala** gly arg lys glu lys pro **ala** asp pro val glu  
trp thr val met asp val val glu tyr phe thr glu  
ala gly phe pro glu gln ala thr ala phe gln glu  
gln glu ile asp gly lys ser leu leu leu met gln  
arg thr asp val leu thr gly leu ser ile arg leu  
gly pro ala leu lys ile tyr glu his his ile lys  
val leu gln gln gly his phe glu asp asp asp pro  
**glu** gly phe leu gly

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
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ATHEROSCLEROSIS

Fig. 3

ala ser ala arg ala ala arg asn lys arg ala  
gly glu glu arg val leu glu lys glu glu glu glu  
glu glu glu glu asp asp glu asp asp asp asp  
val val ser glu gly ser glu val pro glu ser asp  
arg pro ala gly ala gln his his gln leu asn gly  
gly glu arg gly pro gln thr ala lys glu arg ala  
lys glu trp ser leu cys gly pro his pro gly gln  
glu glu gly arg gly pro ala ala gly ser gly thr  
arg gln val phe ser met ala ala leu ser lys glu  
gly gly ser ala ser ser thr thr gly pro asp ser  
pro ser pro val pro leu pro pro gly lys pro ala  
leu pro gly ala asp gly thr pro phe gly cys pro  
ala gly arg lys glu lys pro ala asp pro val glu  
trp thr val met asp val val glu tyr phe thr glu  
ala gly phe pro glu gln ala thr ala phe gln glu  
gln glu ile asp gly lys ser leu leu leu met gln  
arg thr asp val leu thr gly leu ser ile arg leu  
gly pro ala leu lys ile tyr glu his his ile lys  
val leu gln gln gly his phe glu asp asp asp pro  
glu gly phe leu gly

## NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

Fig. 4

thr arg leu gly ala leu ala  
leu pro arg gly asp arg pro gly arg ala pro pro  
ala ala ser ala arg ala ala arg asn lys arg ala  
gly glu glu arg val leu glu lys glu glu glu glu  
**glu glu glu glu asp asp glu asp asp asp asp**  
**val** val ser glu gly ser glu val pro glu ser asp  
arg pro ala gly ala gln his his gln leu asn **gly**  
gly glu arg gly pro gln **thr** ala lys glu arg **ala**  
lys glu trp **ser** leu cys gly pro his **pro** gly gln  
**glu** glu gly arg gly pro ala **ala** gly ser gly thr  
arg gln val phe ser met ala ala **leu ser** lys glu  
gly gly **ser** ala ser **ser thr** thr gly pro asp ser  
pro ser pro val pro leu pro pro gly lys pro ala  
leu pro gly ala asp gly thr pro phe gly cys pro  
**ala** gly arg lys glu lys pro **ala** asp pro val glu  
trp thr val met asp val val glu tyr phe thr glu  
ala gly phe pro glu gln ala thr ala phe gln glu  
gln glu ile asp gly lys ser leu leu leu met gln  
arg thr asp val leu thr gly leu ser ile arg leu  
gly pro ala leu lys ile tyr glu his his ile lys  
val leu gln gln gly his phe glu asp asp asp pro  
**glu** gly phe leu gly

Fig. 5

met lys asn gln  
asp lys lys asn gly ala ala lys gln pro asn pro  
lys ser ser pro gly gln pro glu ala gly ala glu  
gly ala gln gly arg pro gly arg pro ala pro ala  
arg glu ala glu gly ala ser ser gln ala pro gly  
arg pro glu gly ala gln ala lys thr ala gln pro  
gly ala leu cys asp val ser glu glu leu ser arg  
gln leu glu asp ile leu ser thr tyr cys val asp  
asn asn gln gly ala pro gly glu asp gly val gln  
gly glu pro pro glu pro glu asp ala glu lys ser  
arg ala tyr val ala arg asn gly glu pro glu pro  
gly thr pro val val asn gly glu lys glu thr ser  
lys ala glu pro gly thr glu glu ile arg thr ser  
asp glu val gly asp arg asp his arg arg pro gln  
glu lys lys lys ala lys gly leu gly lys glu ile  
thr leu leu met gln thr leu asn thr leu ser thr  
pro glu glu lys leu ala ala leu cys lys lys tyr  
ala glu leu leu glu glu his arg asn ser gln lys  
gln met lys leu leu gln lys lys gln ser gln leu  
val gln glu lys asp his leu arg gly glu his ser  
lys ala ile leu ala arg ser lys leu glu ser leu  
cys arg glu leu gln arg his asn arg ser leu lys  
glu glu gly val gln arg ala arg glu glu glu glu  
lys arg lys glu val thr ser his phe gln met thr  
leu asn asp ile gln leu gln met glu gln his asn  
glu arg asn ser lys leu arg gln glu asn met glu



Fig. 5 (continued)

leu ala glu arg leu lys lys leu ile glu gln tyr  
glu leu arg glu glu his ile asp lys val phe lys  
his lys asp leu gln gln gln leu val asp ala lys  
leu gln gln ala gln glu met leu lys glu ala glu  
glu arg his gln arg glu lys asp phe leu leu lys  
glu ala val glu ser gln arg met cys glu leu met  
lys gln gln glu thr his leu lys gln gln leu ala  
leu tyr thr glu lys phe glu glu phe gln asn thr  
leu ser lys ser ser glu val phe thr thr phe lys  
gln glu met glu lys met thr lys lys ile lys lys  
leu glu lys glu thr thr met tyr arg ser arg trp  
glu ser ser asn lys ala leu leu glu met ala glu  
glu lys thr leu arg asp lys glu leu glu gly leu  
gln val lys ile gln arg leu glu lys leu cys arg  
ala leu gln thr glu arg asn asp leu asn lys arg  
val gln asp leu ser ala gly gly gln gly pro val  
ser asp ser gly pro glu arg arg pro glu pro ala  
thr thr ser lys glu gln gly val glu gly pro gly  
ala gln val pro asn ser pro arg ala thr asp ala  
ser cys cys ala gly ala pro ser thr glu ala ser  
gly gln thr gly pro gln glu pro thr thr ala thr  
ala

Fig. 6

met ser lys asn thr val ser ser ala  
arg phe arg lys val asp val asp glu tyr asp glu  
asn lys phe val asp glu glu asp gly gly asp gly  
gln ala gly pro asp glu gly glu val asp ser cys  
leu arg gln gly asn met thr ala ala leu gln ala  
ala leu lys asn pro pro ile asn thr **lys** ser gln  
ala val lys asp arg ala gly ser ile val leu lys  
val leu ile ser phe lys ala **asn** asp ile glu lys  
ala val gln ser leu asp **lys** asn gly val asp leu  
leu met lys tyr ile tyr lys gly phe glu ser pro  
ser asp asn ser ser ala **met** leu leu gln trp his  
glu lys ala leu ala ala gly gly val gly ser ile  
val arg val leu thr ala arg lys thr val

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
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Fig. 7A (1/3)

atg gcg ggg ccc ccg gcc cta ccc ccg ccg gag acg gcg gcg gcc gcc	48
Met Ala Gly Pro Pro Ala Leu Pro Pro Pro Glu Thr Ala Ala Ala Ala	
1 5 10 15	
acc acg gcg gcc gcc gcc tcg tcg tcc gcc gct tcc ccg cac tac caa	96
Thr Thr Ala Ala Ala Ala Ser Ser Ser Ala Ala Ser Pro His Tyr Gln	
20 25 30	
gag tgg atc ctg gac acc atc gac tcg ctg cgc tcg cgc aag gcg ccg	144
Glu Trp Ile Leu Asp Thr Ile Asp Ser Leu Arg Ser Arg Lys Ala Arg	
35 40 45	
ccg gac ctg gag cgc atc tgc ccg atg gtg ccg ccg ccg cac ggc ccg	192
Pro Asp Leu Glu Arg Ile Cys Arg Met Val Arg Arg Arg His Gly Pro	
50 55 60	
gag ccg gag cgc acg cgc gcc gag ctc gag aaa ctg atc cag cag cgc	240
Glu Pro Glu Arg Thr Arg Ala Glu Leu Glu Lys Leu Ile Gln Gln Arg	
65 70 75 80	
gcc gtg ctc ccg gtc agc tac aag ggg agc atc tcg tac cgc aac gcg	288
Ala Val Leu Arg Val Ser Tyr Lys Gly Ser Ile Ser Tyr Arg Asn Ala	
85 90 95	
gcg cgc gtc cag ccg ccc ccg cgc gga gcc acc ccg ccg gcc ccg ccg	336
Ala Arg Val Gln Pro Pro Arg Arg Gly Ala Thr Pro Pro Ala Pro Pro	
100 105 110	
cgc gcc ccc cgc ggg gcc ccc gcc gcc gcc gcc gcc gcc gcg ccg ccg	384
Arg Ala Pro Arg Gly Ala Pro Ala Ala Ala Ala Ala Ala Ala Pro Pro	
115 120 125	
ccc acg ccc gcc ccg ccg cca ccg ccc gcg ccc gtc gcc gcc gcc gcc	432
Pro Thr Pro Ala Pro Pro Pro Pro Pro Ala Pro Val Ala Ala Ala Ala	
130 135 140	
ccg gcc ccg gcg ccc cgc gcg gcc gcc gcc gcc gcc gcc aca gcg ccc ccc	480
Pro Ala Arg Ala Pro Arg Ala Ala Ala Ala Ala Ala Thr Ala Pro Pro	
145 150 155 160	
tcg cct ggc ccc gcg cag ccg ggc ccc cgc gcg cag ccg gcc gcg ccc	528
Ser Pro Gly Pro Ala Gln Pro Gly Pro Arg Ala Gln Arg Ala Ala Pro	
165 170 175	
ctg gcc gcg ccg ccg ccc gcg cca gcc gct ccc ccg gcg gtg gcg ccc	576
Leu Ala Ala Pro Pro Pro Ala Pro Ala Ala Pro Pro Ala Val Ala Pro	
180 185 190	
ccg gcc ggc ccg cgc cgc gcc ccc ccg ccc gcc gtc gcc gcc ccg gag	624
Pro Ala Gly Pro Arg Arg Ala Pro Pro Pro Ala Val Ala Ala Arg Glu	
195 200 205	
ccg ccg ctg ccg ccg ccg cca cag ccg ccg gcg ccg cca cag cag cag	672
Pro Pro Leu Pro Pro Pro Pro Gln Pro Pro Ala Pro Pro Gln Gln Gln	
210 215 220	

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Fig. 7A (continued; 2/3)

cag ccg ccg ccg ccg cag cca cag ccg ccg ccg gag ggg ggc gcg gtg	720
Gln Pro Pro Pro Pro Gln Pro Gln Pro Pro Pro Glu Gly Gly Ala Val	
225 230 235 240	
cgg gcc ggc ggc gcg gcg cgg ccc gtg agc ctg cgg gaa gtc gtg cgc	768
Arg Ala Gly Gly Ala Ala Arg Pro Val Ser Leu Arg Glu Val Val Arg	
245 250 255	
tac ctc ggg ggc agc ggc ggc gcc ggc ggt cgc cta acc cgc ggc cgc	816
Tyr Leu Gly Gly Ser Gly Gly Ala Gly Gly Arg Leu Thr Arg Gly Arg	
260 265 270	
gtg cag ggg ctg ctg gag gag gag gcg gcg gct cga ggc cgt ctg gag	864
Val Gln Gly Leu Leu Glu Glu Glu Ala Ala Ala Arg Gly Arg Leu Glu	
275 280 285	
cgc acc cgt ctc gga gcg ctt gcg ctg ccc cgc ggg gac agg ccc gga	912
Arg Thr Arg Leu Gly Ala Leu Ala Leu Pro Arg Gly Asp Arg Pro Gly	
290 295 300	
cgg gcg ccg ccg gcc gcc agc gcc cgc ccg tct cgc agc aag aga ggt	960
Arg Ala Pro Pro Ala Ala Ser Ala Arg Pro Ser Arg Ser Lys Arg Gly	
305 310 315 320	
gga gaa gag cga gta ctt gag aaa gaa gag gaa gaa gat gat gat gaa	1008
Gly Glu Glu Arg Val Leu Glu Lys Glu Glu Glu Glu Asp Asp Asp Glu	
325 330 335	
gat gaa gat gaa gaa gat gat gtg tca gag ggc tct gaa gtg ccc gag	1056
Asp Glu Asp Glu Glu Asp Asp Val Ser Glu Gly Ser Glu Val Pro Glu	
340 345 350	
agt gac cgt cct gca ggt gcc cag cac cac cag ctt aac ggc gag cgg	1104
Ser Asp Arg Pro Ala Gly Ala Gln His His Gln Leu Asn Gly Glu Arg	
355 360 365	
gga cct cag agt gcc aag gag agg gtc aag gag tgg acc ccc tgc gga	1152
Gly Pro Gln Ser Ala Lys Glu Arg Val Lys Glu Trp Thr Pro Cys Gly	
370 375 380	
ccg cac cag ggc cag gat gaa ggg cgg ggg cca gcc ccg ggc agc gcc	1200
Pro His Gln Gly Gln Asp Glu Gly Arg Gly Pro Ala Pro Gly Ser Gly	
385 390 395 400	
acc cgc cag gtg ttc tcc atg gca gcc atg aac aag gaa ggg gga aca	1248
Thr Arg Gln Val Phe Ser Met Ala Ala Met Asn Lys Glu Gly Gly Thr	
405 410 415	
gct tct gtt gcc acc ggg cca gac tcc cgg tcc ccc gtg cct ttg ccc	1296
Ala Ser Val Ala Thr Gly Pro Asp Ser Pro Ser Pro Val Pro Leu Pro	
420 425 430	
cca ggc aaa cca gcc cta cct ggg gcc gac ggg acc ccc ttt ggc tgt	1344
Pro Gly Lys Pro Ala Leu Pro Gly Ala Asp Gly Thr Pro Phe Gly Cys	
435 440 445	

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Fig. 7A (continued; 3/3)

ccg ccc ggg cgc aaa gag aag cca tct gat ccc gtc gag tgg acc gtg	1392
Pro Pro Gly Arg Lys Glu Lys Pro Ser Asp Pro Val Glu Trp Thr Val	
450 455 460	
atg gat gtc gtc gaa tat ttt act gag gct gga ttc ccg gag cag gcg	1440
Met Asp Val Val Glu Tyr Phe Thr Glu Ala Gly Phe Pro Glu Gln Ala	
465 470 475 480	
aca gct ttc caa gag cag gaa att gat ggc aaa tct ttg ctg ctc atg	1488
Thr Ala Phe Gln Glu Gln Glu Ile Asp Gly Lys Ser Leu Leu Leu Met	
485 490 495	
cag cgc aca gat gtg ctc acc ggc ctg tcc atc cgc ctc ggg cca gcc	1536
Gln Arg Thr Asp Val Leu Thr Gly Leu Ser Ile Arg Leu Gly Pro Ala	
500 505 510	
ctg aaa atc tac gag cac cac atc aag gtg ctt cag caa ggc cac ttt	1584
Leu Lys Ile Tyr Glu His His Ile Lys Val Leu Gln Gln Gly His Phe	
515 520 525	
gag gat gat gac ccc gat ggc ttc tta ggc	1614
Glu Asp Asp Asp Pro Asp Gly Phe Leu Gly	
530 535	

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Fig. 7B

glu glu arg val leu glu lys glu glu glu glu **asp**  
**asp asp** glu asp **glu asp glu glu** asp asp val ser  
glu gly ser glu val pro glu ser asp arg pro ala  
gly ala gln his his gln leu asn gly glu arg gly  
pro gln **ser** ala lys glu arg **val** lys glu trp **thr**  
**pro** cys gly pro his **gln** gly gln **asp** glu gly arg  
gly pro ala **pro** gly ser gly thr arg gln val phe  
ser met ala ala **met asn** lys glu gly gly **thr** ala  
ser **val ala** thr gly pro asp ser pro ser pro val  
pro leu pro pro gly lys pro ala leu pro gly ala  
asp gly thr pro phe gly cys pro **pro** gly arg lys  
glu lys pro **ser** asp pro val glu trp thr val met  
asp val val glu tyr phe thr glu ala gly phe pro  
glu gln ala thr ala phe gln glu gln glu ile asp  
gly lys ser leu leu leu met gln arg thr asp val  
leu thr gly leu ser ile arg leu gly pro ala leu  
lys ile tyr glu his his ile lys val leu gln gln  
gly his phe glu asp asp asp pro **asp** gly phe leu  
gly

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# NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

Fig. 8A (1/3)

atg	aag	aac	caa	gac	aaa	aag	aac	ggg	gct	gcc	aaa	caa	tcc	aat	cca	48
Met	Lys	Asn	Gln	Asp	Lys	Lys	Asn	Gly	Ala	Ala	Lys	Gln	Ser	Asn	Pro	
1				5					10					15		
aaa	agc	agc	cca	gga	caa	ccg	gaa	gca	gga	ccc	gag	gga	gcc	cag	gag	96
Lys	Ser	Ser	Pro	Gly	Gln	Pro	Glu	Ala	Gly	Pro	Glu	Gly	Ala	Gln	Glu	
			20					25					30			
cgg	ccc	agc	cag	gcg	gct	cct	gca	gta	gaa	gca	gaa	ggt	ccc	ggc	agc	144
Arg	Pro	Ser	Gln	Ala	Ala	Pro	Ala	Val	Glu	Ala	Glu	Gly	Pro	Gly	Ser	
		35					40					45				
agc	cag	gct	cct	cgg	aag	ccg	gag	ggt	gct	caa	gcc	aga	acg	gct	cag	192
Ser	Gln	Ala	Pro	Arg	Lys	Pro	Glu	Gly	Ala	Gln	Ala	Arg	Thr	Ala	Gln	
	50					55					60					
tct	ggg	gcc	ctt	cgt	gat	gtc	tct	gag	gag	ctg	agc	cgc	caa	ctg	gaa	240
Ser	Gly	Ala	Leu	Arg	Asp	Val	Ser	Glu	Glu	Leu	Ser	Arg	Gln	Leu	Glu	
65				70						75					80	
gac	ata	ctg	agc	aca	tac	tgt	gtg	gac	aat	aac	cag	ggg	ggc	ccc	ggc	288
Asp	Ile	Leu	Ser	Thr	Tyr	Cys	Val	Asp	Asn	Asn	Gln	Gly	Gly	Pro	Gly	
				85					90					95		
gag	gat	ggg	gca	cag	ggt	gag	ccg	gct	gaa	ccc	gaa	gat	gca	gag	aag	336
Glu	Asp	Gly	Ala	Gln	Gly	Glu	Pro	Ala	Glu	Pro	Glu	Asp	Ala	Glu	Lys	
			100					105					110			
tcc	cgg	acc	tat	gtg	gca	agg	aat	ggg	gag	cct	gaa	cca	act	cca	gta	384
Ser	Arg	Thr	Tyr	Val	Ala	Arg	Asn	Gly	Glu	Pro	Glu	Pro	Thr	Pro	Val	
		115					120					125				
gtc	aat	gga	gag	aag	gaa	ccc	tcc	aag	ggg	gat	cca	aac	aca	gaa	gag	432
Val	Asn	Gly	Glu	Lys	Glu	Pro	Ser	Lys	Gly	Asp	Pro	Asn	Thr	Glu	Glu	
	130					135					140					
atc	cgg	cag	agt	gac	gag	gtc	gga	gac	cga	gac	cat	cga	agg	cca	cag	480
Ile	Arg	Gln	Ser	Asp	Glu	Val	Gly	Asp	Arg	Asp	His	Arg	Arg	Pro	Gln	
145				150						155					160	
gag	aag	aaa	aaa	gcc	aag	ggt	ttg	ggt	aag	gag	atc	acg	ttg	ctg	atg	528
Glu	Lys	Lys	Lys	Ala	Lys	Gly	Leu	Gly	Lys	Glu	Ile	Thr	Leu	Leu	Met	
				165					170					175		
cag	aca	ttg	aat	act	ctg	agt	acc	cca	gag	gag	aag	ctg	gct	gct	ctg	576
Gln	Thr	Leu	Asn	Thr	Leu	Ser	Thr	Pro	Glu	Glu	Lys	Leu	Ala	Ala	Leu	
			180					185					190			
tgc	aag	aag	tat	gct	gaa	ctg	ctg	gag	gag	cac	cgg	aat	tca	cag	aag	624
Cys	Lys	Lys	Tyr	Ala	Glu	Leu	Leu	Glu	Glu	His	Arg	Asn	Ser	Gln	Lys	
		195					200					205				

# NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

Fig. 8A (continued; 2/3)

cag Gln 210	atg Met	aag Lys	ctc Leu	cta Leu	cag Gln 215	aaa Lys	aag Lys	cag Gln	agc Ser	cag Gln	ctg Leu 220	gtg Val	caa Gln	gag Glu	aag Lys	672
gac Asp 225	cac His	ctg Leu	cgc Arg	ggt Gly 230	gag Glu 230	cac His	agc Ser	aag Lys	gcc Ala	gtc Val 235	ctg Leu 235	gcc Ala	cgc Arg	agc Ser	aag Lys 240	720
ctt Leu	gag Glu	agc Ser	cta Leu 245	tgc Cys 245	cgt Arg	gag Glu	ctg Leu	cag Gln 250	cgg Arg 250	cac His	aac Asn 250	cgc Arg	tcc Ser 255	ctc Leu 255	aag Lys	768
gaa Glu 260	gaa Glu	ggt Gly 260	gtg Val 260	cag Gln 260	cgg Arg	gcc Ala	cgg Arg	gag Glu 265	gag Glu 265	gag Glu 265	gag Glu 265	aag Lys 270	cgc Arg 270	aag Lys	gag Glu	816
gtg Val 275	acc Thr	tcg Ser 275	cac His	ttc Phe	cag Gln 280	gtg Val 280	aca Thr 280	ctg Leu 280	aat Asn 280	gac Asp 285	att Ile 285	cag Gln 285	ctg Leu 285	cag Gln	atg Met	864
gaa Glu 290	cag Gln 290	cac His	aat Asn 290	gag Glu 295	cgc Arg 295	aac Asn 295	tcc Ser 295	aag Lys 295	ctg Leu 300	cgc Arg 300	caa Gln 300	gag Glu 300	aac Asn 300	atg Met	gag Glu	912
ctg Leu 305	gct Ala	gag Glu	agg Arg	ctc Leu 310	aag Lys 310	aag Lys	ctg Leu	att Ile	gag Glu 315	cag Gln 315	tat Tyr 315	gag Glu 315	ctg Leu 315	cgc Arg	gag Glu 320	960
gag Glu 325	cat His	atc Ile	gac Asp 325	aaa Lys 325	gtc Val 325	ttc Phe 330	aaa Lys	cac His 330	aag Lys 330	gac Asp 330	cta Leu 335	caa Gln 335	cag Gln 335	cag Gln 335	ctg Leu 335	1008
gtg Val 340	gat Asp	gcc Ala	aag Lys 340	ctc Leu 340	cag Gln 345	cag Gln 345	gcc Ala 345	cag Gln 345	gag Glu 345	atg Met 350	cta Leu 350	aag Lys 350	gag Glu 350	gca Ala	gaa Glu	1056
gag Glu 355	cgg Arg	cac His 355	cag Gln 355	cgg Arg	gag Glu 360	aag Lys 360	gat Asp 360	ttt Phe 360	ctc Leu 365	ctg Leu 365	aaa Lys 365	gag Glu 365	gca Ala	gta Val	gag Glu	1104
tcc Ser 370	cag Gln 370	agg Arg	atg Met	tgt Cys	gag Glu 375	ctg Leu 375	atg Met 375	aag Lys 375	cag Gln 380	caa Gln 380	gag Glu 380	acc Thr 380	cac His	ctg Leu 385	aag Lys	1152
caa Gln 385	cag Gln 385	ctt Leu	gcc Ala	cta Leu 390	tac Tyr 390	aca Thr 390	gag Glu 390	aag Lys 395	ttt Phe 395	gag Glu 395	gag Glu 395	ttc Phe 395	cag Gln 400	aac Asn	aca Thr 400	1200
ctt Leu	tcc Ser	aaa Lys	agc Ser 405	agc Ser 405	gag Glu 405	gta Val	ttc Phe	acc Thr 410	aca Thr 410	ttc Phe 410	aag Lys 410	cag Gln 415	gag Glu 415	atg Met	gaa Glu	1248



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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
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ATHEROSCLEROSIS

Fig. 8A (continued; 3/3)

aag atg act aag aag atc aag aag ctg gag aaa gaa acc acc atg tac	1296
Lys Met Thr Lys Lys Ile Lys Lys Leu Glu Lys Glu Thr Thr Met Tyr	
420 425 430	
cgg tcc cgg tgg gag agc agc aac aag gcc ctg ctt gag atg gct gag	1344
Arg Ser Arg Trp Glu Ser Ser Asn Lys Ala Leu Leu Glu Met Ala Glu	
435 440 445	
gag aaa aca gtc cgg gat aaa gaa ctg gag ggc ctg cag gta aaa atc	1392
Glu Lys Thr Val Arg Asp Lys Glu Leu Glu Gly Leu Gln Val Lys Ile	
450 455 460	
caa cgg ctg gag aag ctg tgc cgg gca ctg cag aca gag cgc aat gac	1440
Gln Arg Leu Glu Lys Leu Cys Arg Ala Leu Gln Thr Glu Arg Asn Asp	
465 470 475 480	
ctg aac aag agg gta cag gac ctg agt gct ggt ggc cag ggc tcc ctc	1488
Leu Asn Lys Arg Val Gln Asp Leu Ser Ala Gly Gly Gln Gly Ser Leu	
485 490 495	
act gac agt ggc cct gag agg agg cca gag ggg cct ggg gct caa gca	1536
Thr Asp Ser Gly Pro Glu Arg Arg Pro Glu Gly Pro Gly Ala Gln Ala	
500 505 510	
ccc agc tcc ccc agg gtc aca gaa gcg cct tgc tac cca gga gca ccg	1584
Pro Ser Ser Pro Arg Val Thr Glu Ala Pro Cys Tyr Pro Gly Ala Pro	
515 520 525	
agc aca gaa gca tca ggc cag act ggg cct caa gag ccc acc tcc gcc	1632
Ser Thr Glu Ala Ser Gly Gln Thr Gly Pro Gln Glu Pro Thr Ser Ala	
530 535 540	
agg gcc	1638
Arg Ala	
545	

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS

Fig. 8 B

lys ser ser pro gly gln pro glu ala gly pro glu gly ala  
gln glu arg pro ser gln ala ala pro ala val glu ala glu gly  
pro gly ser ser gln ala pro arg lys pro glu gly ala gln ala  
arg thr ala gln ser gly ala leu arg asp val ser glu glu leu  
ser arg gln leu glu asp ile leu ser thr tyr cys val asp asn  
asn gln gly gly pro gly glu asp gly ala gln gly glu pro ala  
glu pro glu asp ala glu lys ser arg thr tyr val ala arg asn  
gly glu pro glu pro thr pro val val tyr gly glu lys glu pro  
ser lys gly asp pro asn thr glu glu ile arg gln ser asp glu  
val gly asp arg asp his arg arg pro gln glu lys lys lys ala  
lys gly leu gly lys glu ile thr leu leu met gln thr leu asn  
thr leu ser thr pro glu glu lys leu ala ala leu cys lys lys  
tyr ala glu leu leu glu glu his arg asn ser gln lys gln met  
lys leu leu gln lys lys gln ser gln leu val gln glu lys asp  
his leu arg gly glu his ser lys ala val leu ala arg ser lys  
leu glu ser leu cys arg glu leu gln arg his asn arg ser leu  
lys glu glu gly val gln arg ala arg glu glu glu glu lys arg  
lys glu val thr ser his phe gln val thr leu asn asp ile gln  
leu gln met glu gln his asn glu arg asn ser lys leu arg gln  
glu asn met glu leu ala glu arg leu lys lys leu ile glu gln  
tyr glu leu arg glu glu his ile asp lys val phe lys his lys  
asp leu gln gln gln leu val asp ala lys leu gln gln ala gln  
glu met leu lys glu ala glu glu arg his gln arg glu lys asp  
phe leu leu lys glu ala val glu ser gln arg met cys glu leu  
met lys gln gln glu thr his leu lys gln gln leu ala leu tyr  
thr glu lys phe glu glu phe gln asn thr leu ser lys ser ser

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Fig. 8 B(continued)

glu val phe thr thr phe lys gln glu met glu lys met thr lys  
lys ile lys lys leu glu lys glu thr thr met tyr arg ser arg  
trp glu ser ser asn lys ala leu leu glu met ala glu glu lys  
thr val arg asp lys glu leu glu gly leu gln val lys ile gln  
arg leu glu lys leu cys arg ala leu gln thr glu arg asn asp  
leu asn lys arg val gln asp leu ser ala gly gly gln gly ser  
leu thr asp ser gly pro glu arg arg pro glu gly pro gly ala  
gln ala pro ser ser pro arg val thr glu ala pro cys tyr pro  
gly ala pro ser thr glu ala ser gly gln thr gly pro gln glu  
pro thr ser ala arg ala \*\*\*

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
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Fig. 9

val asp val asp

glu tyr asp glu asn lys phe val asp glu glu asp

gly gly asp gly

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Fig. 10

1 AAG CCT CGC AGC GGT CGG GGC GGC GCC GCG GAG GCT  
37 CGA GGG CGG CGG GCG GCG GCG ATG TCG AAG AAC ACG  
met ser lys asn thr

73 GTG TCG TCG GCG CGG TTC CGG AAG GTG GAC GTG GAT  
val ser ser ala arg phe arg lys val asp val asp

109 GAG TAC GAC GAG AAC AAG TTC GTG GAC GAG GAA GAC  
glu tyr asp glu asn lys phe val asp glu glu asp

145 GGC GGC GAC GGC CAG GCG GGG CCG GAC GAG GGC GAG  
gly gly asp gly gln ala gly pro asp glu gly glu

181 GTG GAC TCG TGC CTG CGG CAA GGG AAC ATG ACA GCC  
val asp ser cys leu arg gln gly asn met thr ala

217 GCC CTG CAG GCG GCG CTG AAG AAC CCT CCC ATC AAC  
ala leu gln ala ala leu lys asn pro pro ile asn

253 ACC AGG AGC CAG GCG GTG AAG GAC CGG GCA GGC AGC  
thr **arg** ser gln ala val lys asp arg ala gly ser

289 ATC GTG CTG AAG GTG CTC ATC TCC TTC AAG GCC GGC  
ile val leu lys val leu ile ser phe lys ala **gly**

325 GAC ATA GAA AAG GCC GTG CAG TCC CTG GAC AGG AAC  
asp ile glu lys ala val gln ser leu asp **arg** asn

361 GGC GTG GAC CTG CTC ATG AAG TAC ATC TAC AAG GGC  
gly val asp leu leu met lys tyr ile tyr lys gly

397 TTC GAG AGC CCC TCC GAC AAC AGC AGC GCC GTG CTC  
phe glu ser pro ser asp asn ser ser ala **val** leu

433 CTG CAG TGG CAC GAG AAG GCG CTG GCT GCA GGA GGA  
leu gln trp his glu lys ala leu ala ala gly gly

469 GTG GGC TCC ATC GTC CGT GTC CTG ACT GCA AGG AAA  
val gly ser ile val arg val leu thr ala arg lys

505 ACC GTG TAG CCT GGC AGG AAC GGG TGC CTG CCG GGG  
thr val

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
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Fig. 10 (continued)

541 AGC GGG AGC TGC CGG TAC AAA GAC CAA AAC GCC CAG  
577 ATG CCG CCG CTG CCC TGT GGG CGG CGT CTG TTC CCA  
613 GCT TCG CTT TTT CCC TTT CCC GTG TCT GTC AGG ATT  
649 ACA TAA GGT TTC CCT TCG TGA GAA TCG GAG TGG CGC  
685 AGA GGG TCC TGT TCA TAC GCG CCG TGC GTC CGG CTG  
721 TGT AAG ACC CCT GCC TTC AGT GTC CTT GAG CAA CGG  
757 TAG CGT GTC GCC GGC TGG GTT TGG TTT TGT CGT GGA  
793 GGG ATC TGG TCA GAA TTT GAG GCC AGT TTC CTA ACT  
829 CAT TGC TGG TCA GGA AAT GAT CTT CAT TTA AAA AAA  
865 AAA AAA AGA CTG GCA GCT ATT ATG CAA AAC TGG ACC  
901 CTC TTC CCT TAT TTA AGC AGA GTG AGT TTC TGG AAC  
937 CAG TGG TGC CCC CCC CCC CGC CCC GGC CGC CGT CCT  
973 GCT CAA GGG AAG CCT CCC TGC AGA GCA GCA GAG CCC  
1009 CTG GGC AGG AGC GCC GCG TCC CGC TCC CAG GAG ACA  
1045 GCA TGC GCG GTC ACG CGG CAC TTC CTG TGC CTC CCA  
1081 GCC CCA GTG CCC CGG AGT TCT TCA GGG CGA CAG GGA  
1117 CCT CAG AAG ACT GGA TCC GAT CCA GAC AGA CGC CCA  
1153 TTC TTG GTT CAG CTC AGT GTT TTC AAA AGG AAC GTG  
1189 CTA CCG TGG GTA GAG CAC ACT GGT TCT CAG AAC ACG  
1225 GCC GGC GCT TGA CGG TTG TCA CAG CTC CAG AAC AAA  
1261 TCC TGG GAG ACA GGC GAG CGC GAG TCG CCG GGC AGG  
1297 AAT TCC ACA CAC TCG TGC TGT TTT TGA TAC CTG CTT  
1333 TTT GTT TTG TTT TGT AAA AAT GAT GCA CTT GAG AAA  
1369 ATA AAA CGT CAG TGT TGA CAA AAA AAA AAA AAA AAA

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
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Fig. 11

1 GAC TGC CGC AGC AGC AGC AAC AAC CGC TAG CCG AAG  
asp cys arg ser ser ser asn asn arg Xaa pro lys

37 GGT GGC GCG GCG CGG GCC GGC GGC CCG GCG CGG CCC  
gly gly ala ala arg ala gly gly pro ala arg pro

73 GTG AGC CTG CGG GAA GTC GTG CGC TAC CTC GGG GGT  
val ser leu arg glu val val arg tyr leu gly gly

109 AGC AGC GGC GCT GGC GGC CGC CTG ACC CGC GGC CGC  
ser ser gly ala gly gly arg leu thr arg gly arg

145 GTG CAG GGT CTG CTG GAA GAG GAG GCG GCG GCG CGG  
val gln gly leu leu glu glu glu ala ala ala arg

181 GGC CGC CTG GAG CGC ACC CGT CTC GGA GCG CTT GCG  
gly arg leu glu arg thr arg leu gly ala leu ala

217 CTG CCC CGC GGG GAC AGG CCC GGA CGG GCG CCA CCG  
leu pro arg gly asp arg pro gly arg ala pro pro

253 GCC GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT  
ala ala ser ala arg ala ala arg asn lys arg ala

289 GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG GAG  
gly glu glu arg val leu glu lys glu glu glu glu

325 GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC GAC  
**glu glu glu** glu asp **asp glu asp asp** asp asp **asp**

361 GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT  
**val** val ser glu gly ser glu val pro glu ser asp

397 CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC  
arg pro ala gly ala gln his his gln leu asn **gly**

433 GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC  
gly glu arg gly pro gln **thr** ala lys glu arg **ala**

469 AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG  
lys glu trp **ser leu** cys gly pro his **pro** gly gln

Fig. 11 (continued)

505 GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC  
glu glu gly arg gly pro ala ala gly ser gly thr

541 CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG  
arg gln val phe ser met ala ala leu ser lys glu

577 GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC  
gly gly ser ala ser ser thr thr gly pro asp ser

613 CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC  
pro ser pro val pro leu pro pro gly lys pro ala

649 CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT  
leu pro gly ala asp gly thr pro phe gly cys pro

685 GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG  
ala gly arg lys glu lys pro ala asp pro val glu

721 TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG  
trp thr val met asp val val glu tyr phe thr glu

757 GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG  
ala gly phe pro glu gln ala thr ala phe gln glu

793 CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG  
gln glu ile asp gly lys ser leu leu leu met gln

829 CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG  
arg thr asp val leu thr gly leu ser ile arg leu

865 GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG  
gly pro ala leu lys ile tyr glu his his ile lys

901 GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG  
val leu gln gln gly his phe glu asp asp asp pro

937 GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC  
glu gly phe leu gly

973 CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC

1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG

1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC

1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT



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Fig. 11 (continued)

1117	TGC	TAC	CCC	CCC	ACC	CCG	TGT	GTG	TCT	CTG	CAC	CTG
1153	CCC	CCA	GCA	CAC	CCC	TCC	CGG	AGC	CTG	GAT	GTC	GCC
1189	TGG	GAC	TCT	GGC	CTG	CTC	ATT	TTG	CCC	CCA	GAT	CAG
1225	CCC	CCT	CCC	TCC	CTC	CTG	TCC	CAG	GAC	ATT	TTT	TAA
1261	AAG	AAA	AAA	AGG	AAA	AAA	AAA	AAT	TGG	GGA	GGG	GGC
1297	TGG	GAA	GGT	GCC	CCA	AGA	TCC	TCC	TCG	GCC	CAA	CCA
1333	GGT	GTT	TAT	TCC	TAT	ATA	TAT	ATA	TAT	ATG	TTT	TGT
1369	TCT	GCC	TGT	TTT	TCG	TTT	TTT	GGT	GCG	TGG	CCT	TTC
1405	TTC	CCT	CCC	ACC	ACC	ACT	CAT	GGC	CCC	AGC	CCT	GCT
1441	CGC	CCT	GTC	GGC	GGG	AGC	AGC	TGG	GAA	TGG	GAG	GAG
1477	GGT	GGG	ACC	TTG	GGT	CTG	TCT	CCC	ACC	CTC	TCT	CCC
1513	GTT	GGT	TCT	GTT	GTC	GCT	CCA	GCT	GGC	TGT	ATT	GCT
1549	TTT	TAA	TAT	TGC	ACC	GAA	GGG	TTG	TTT	TTT	TTT	TTT
1585	TAA	ATA	AAA	TTT	TAA	AAA	AAG	GAA	AAA	AAA	AAA	AAA

Fig. 12

256 GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT  
ala ser ala arg ala ala arg asn lys arg ala

289 GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG GAG  
gly glu glu arg val leu glu lys glu glu glu glu

325 GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC GAC  
**glu glu glu** glu asp **asp glu asp asp** asp asp **asp**

361 GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT  
**val** val ser glu gly ser glu val pro glu ser asp

397 CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC  
arg pro ala gly ala gln his his gln leu asn **gly**

433 GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC  
gly glu arg gly pro gln **thr** ala lys glu arg **ala**

469 AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG  
lys glu trp **ser leu** cys gly pro his **pro** gly gln

505 GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC  
**glu** glu gly arg gly pro ala **ala** gly ser gly thr

541 CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG  
arg gln val phe ser met ala ala **leu ser** lys glu

577 GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC  
gly gly **ser** ala ser **ser thr** thr gly pro asp ser

613 CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC  
pro ser pro val pro leu pro pro gly lys pro ala

649 CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT  
leu pro gly ala asp gly thr pro phe gly cys pro

685 GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG  
**ala** gly arg lys glu lys pro **ala** asp pro val glu

721 TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG  
trp thr val met asp val val glu tyr phe thr glu

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Fig. 12 (continued)

757 GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG  
ala gly phe pro glu gln ala thr ala phe gln glu

793 CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG  
gln glu ile asp gly lys ser leu leu leu met gln

829 CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG  
arg thr asp val leu thr gly leu ser ile arg leu

865 GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG  
gly pro ala leu lys ile tyr glu his his ile lys

901 GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG  
val leu gln gln gly his phe glu asp asp asp pro

937 GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC  
**glu** gly phe leu gly

973 CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC

1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG

1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC

1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT

1117 TGC TAC CCC CCC ACC CCG TGT GTG TCT CTG CAC CTG

1153 CCC CCA GCA CAC CCC TCC CGG AGC CTG GAT GTC GCC

1189 TGG GAC TCT GGC CTG CTC ATT TTG CCC CCA GAT CAG

1225 CCC CCT CCC TCC CTC CTG TCC CAG GAC ATT TTT TAA

1261 AAG AAA AAA AGG AAA AAA AAA AAT TGG GGA GGG GGC

1297 TGG GAA GGT GCC CCA AGA TCC TCC TCG GCC CAA CCA

1333 GGT GTT TAT TCC TAT ATA TAT ATA TAT ATG TTT TGT

1369 TCT GCC TGT TTT TCG TTT TTT GGT GCG TGG CCT TTC

1405 TTC CCT CCC ACC ACC ACT CAT GGC CCC AGC CCT GCT

1441 CGC CCT GTC GGC GGG AGC AGC TGG GAA TGG GAG GAG

1477 GGT GGG ACC TTG GGT CTG TCT CCC ACC CTC TCT CCC

1513 GTT GGT TCT GTT GTC GCT CCA GCT GGC TGT ATT GCT

1549 TTT TAA TAT TGC ACC GAA GGG TTG TTT TTT TTT TTT

1585 TAA ATA AAA TTT TAA AAA AAG GAA AAA AAA AAA

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Fig. 13

196 ACC CGT CTC GGA GCG CTT GCG  
thr arg leu gly ala leu ala

217 CTG CCC CGC GGG GAC AGG CCC GGA CGG GCG CCA CCG  
leu pro arg gly asp arg pro gly arg ala pro pro

253 GCC GCC AGC GCC CGC GCG GCG CGG AAC AAG AGA GCT  
ala ala ser ala arg ala ala arg asn lys arg ala

289 GGC GAG GAG CGA GTG CTT GAA AAG GAG GAG GAG GAG  
gly glu glu arg val leu glu lys glu glu glu glu

325 GAG GAG GAG GAA GAC GAC GAG GAC GAC GAC GAC GAC  
**glu glu glu** glu asp **asp glu asp asp** asp asp **asp**

361 GTC GTG TCC GAG GGC TCG GAG GTG CCC GAG AGC GAT  
**val** val ser glu gly ser glu val pro glu ser asp

397 CGT CCC GCG GGT GCG CAG CAT CAC CAG CTG AAT GGC  
arg pro ala gly ala gln his his gln leu asn **gly**

433 GGC GAG CGC GGC CCG CAG ACC GCC AAG GAG CGG GCC  
gly glu arg gly pro gln **thr** ala lys glu arg **ala**

469 AAG GAG TGG TCG CTG TGT GGC CCC CAC CCT GGC CAG  
lys glu trp **ser leu** cys gly pro his **pro** gly gln

505 GAG GAA GGG CGG GGG CCG GCC GCG GGC AGT GGC ACC  
**glu** glu gly arg gly pro ala **ala** gly ser gly thr

541 CGC CAG GTG TTC TCC ATG GCG GCC TTG AGT AAG GAG  
arg gln val phe ser met ala ala **leu ser** lys glu

577 GGG GGA TCA GCC TCT TCG ACC ACC GGG CCT GAC TCC  
gly gly **ser** ala ser **ser thr** thr gly pro asp ser

613 CCG TCC CCG GTG CCT TTG CCC CCC GGG AAG CCA GCC  
pro ser pro val pro leu pro pro gly lys pro ala

649 CTC CCA GGA GCC GAT GGG ACC CCC TTT GGC TGC CCT  
leu pro gly ala asp gly thr pro phe gly cys pro

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
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ATHEROSCLEROSIS

Fig. 13 (continued)

685 GCC GGG CGC AAA GAG AAG CCG GCA GAC CCC GTG GAG  
 ala gly arg lys glu lys pro ala asp pro val glu  
 721 TGG ACA GTC ATG GAC GTC GTG GAG TAC TTC ACC GAG  
 trp thr val met asp val val glu tyr phe thr glu  
 757 GCG GGC TTC CCT GAG CAA GCC ACG GCT TTC CAG GAG  
 ala gly phe pro glu gln ala thr ala phe gln glu  
 793 CAG GAG ATC GAC GGC AAG TCC CTG CTG CTC ATG CAG  
 gln glu ile asp gly lys ser leu leu leu met gln  
 829 CGC ACC GAT GTC CTC ACC GGC CTG TCC ATC CGC CTG  
 arg thr asp val leu thr gly leu ser ile arg leu  
 865 GGG CCA GCG TTG AAA ATC TAT GAG CAC CAT ATC AAG  
 gly pro ala leu lys ile tyr glu his his ile lys  
 901 GTG CTG CAG CAG GGT CAC TTC GAG GAC GAT GAC CCG  
 val leu gln gln gly his phe glu asp asp asp pro  
 937 GAA GGC TTC CTG GGA TGA GCA CAG AGC CGC CGC GCC  
 glu gly phe leu gly  
 973 CCT TGT CCC CAC CCC CAC CCC GCC TGG ACC CAT TCC  
 1009 TGC CTC CAT GTC ACC CAA GGT GTC CCA GAG GCC AGG  
 1045 AGC TGG ACT GGG CAG GCG AGG GGT GCG GAC CTA CCC  
 1081 TGA TTC TGG TAG GGG GCG GGG CCT TGC TGT GCT CAT  
 1117 TGC TAC CCC CCC ACC CCG TGT GTG TCT CTG CAC CTG  
 1153 CCC CCA GCA CAC CCC TCC CGG AGC CTG GAT GTC GCC  
 1189 TGG GAC TCT GGC CTG CTC ATT TTG CCC CCA GAT CAG  
 1225 CCC CCT CCC TCC CTC CTG TCC CAG GAC ATT TTT TAA  
 1261 AAG AAA AAA AGG AAA AAA AAA AAT TGG GGA GGG GGC  
 1297 TGG GAA GGT GCC CCA AGA TCC TCC TCG GCC CAA CCA  
 1333 GGT GTT TAT TCC TAT ATA TAT ATA TAT ATG TTT TGT  
 1369 TCT GCC TGT TTT TCG TTT TTT GGT GCG TGG CCT TTC  
 1405 TTC CCT CCC ACC ACC ACT CAT GGC CCC AGC CCT GCT  
 1441 CGC CCT GTC GGC GGG AGC AGC TGG GAA TGG GAG GAG  
 1477 GGT GGG ACC TTG GGT CTG TCT CCC ACC CTC TCT CCC  
 1513 GTT GGT TCT GTT GTC GCT CCA GCT GGC TGT ATT GCT  
 1549 TTT TAA TAT TGC ACC GAA GGG TTG TTT TTT TTT TTT  
 1585 TAA ATA AAA TTT TAA AAA AAG GAA AAA AAA AAA

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Fig. 14

1	GTG	GAA	AAT	AGC	AAC	TGT	GTT	TCT	CAA	GGA	TCC	AAT
37	CCC	AAC	CTA	AGG	TGG	CAG	CGC	ACA	ATG	AAG	AAT	CAA
									met	lys	asn	gln
73	GAC	AAA	AAG	AAC	GGG	GCT	GCC	AAA	CAG	CCC	AAC	CCC
	asp	lys	lys	asn	gly	ala	ala	lys	gln	pro	asn	pro
109	AAA	AGC	AGC	CCG	GGA	CAG	CCG	GAA	GCA	GGA	GCG	GAG
	lys	ser	ser	pro	gly	gln	pro	glu	ala	gly	ala	glu
145	GGA	GCC	CAG	GGG	CGG	CCC	GGC	CGG	CCG	GCC	CCC	GCC
	gly	ala	gln	gly	arg	pro	gly	arg	pro	ala	pro	ala
181	CGA	GAA	GCC	GAA	GGT	GCC	AGC	AGC	CAG	GCT	CCC	GGG
	arg	glu	ala	glu	gly	ala	ser	ser	gln	ala	pro	gly
217	AGG	CCG	GAG	GGG	GCT	CAA	GCC	AAA	ACT	GCT	CAG	CCT
	arg	pro	glu	gly	ala	gln	ala	lys	thr	ala	gln	pro
253	GGG	GCG	CTC	TGT	GAT	GTC	TCT	GAG	GAG	CTG	AGC	CGC
	gly	ala	leu	cys	asp	val	ser	glu	glu	leu	ser	arg
289	CAG	TTG	GAA	GAC	ATA	CTC	AGT	ACA	TAC	TGT	GTG	GAC
	gln	leu	glu	asp	ile	leu	ser	thr	tyr	cys	val	asp
325	AAC	AAC	CAG	GGG	GCC	CCG	GGT	GAG	GAT	GGG	GTC	CAG
	asn	asn	gln	gly	ala	pro	gly	glu	asp	gly	val	gln
361	GGT	GAG	CCC	CCT	GAA	CCT	GAA	GAT	GCA	GAG	AAG	TCT
	gly	glu	pro	pro	glu	pro	glu	asp	ala	glu	lys	ser
397	CGC	GCC	TAT	GTG	GCA	AGG	AAT	GGG	GAG	CCG	GAG	CCG
	arg	ala	tyr	val	ala	arg	asn	gly	glu	pro	glu	pro
433	GGC	ACC	CCA	GTA	GTC	AAT	GGC	GAG	AAG	GAG	ACC	TCC
	gly	thr	pro	val	val	asn	gly	glu	lys	glu	thr	ser
469	AAG	GCA	GAG	CCG	GGC	ACG	GAA	GAG	ATC	CGG	ACG	AGC
	lys	ala	glu	pro	gly	thr	glu	glu	ile	arg	thr	ser
505	GAT	GAG	GTC	GGA	GAC	CGA	GAC	CAC	CGG	AGG	CCA	CAG
	asp	glu	val	gly	asp	arg	asp	his	arg	arg	pro	gln

Fig. 14 (continued)

541 GAA AAG AAG AAG GCC AAG GGT CTG GGA AAG GAG ATC  
glu lys lys lys ala lys gly leu gly lys glu ile

577 ACG CTG CTG ATG CAG ACA CTG AAC ACG CTG AGC ACC  
thr leu leu met gln thr leu asn thr leu ser thr

613 CCA GAG GAG AAG CTG GCG GCT CTG TGC AAG AAG TAT  
pro glu glu lys leu ala ala leu cys lys lys tyr

649 GCG GAA CTG CTC GAG GAG CAC CGG AAC TCG CAG AAG  
ala glu leu leu glu glu his arg asn ser gln lys

685 CAG ATG AAG CTG CTG CAG AAG AAG CAG AGC CAG CTG  
gln met lys leu leu gln lys lys gln ser gln leu

721 GTG CAG GAG AAG GAC CAC CTG CGT GGC GAG CAC AGC  
val gln glu lys asp his leu arg gly glu his ser

757 AAG GCC ATC CTG GCC CGC AGC AAG CTC GAG AGC CTG  
lys ala ile leu ala arg ser lys leu glu ser leu

793 TGC CGG GAG CTG CAG CGG CAC AAC CGC TCG CTC AAG  
cys arg glu leu gln arg his asn arg ser leu lys

829 GAA GAA GGT GTG CAG CGA GCC CGA GAG GAG GAG GAG  
glu glu gly val gln arg ala arg glu glu glu glu

865 AAG CGC AAG GAG GTG ACG TCA CAC TTC CAG ATG ACG  
lys arg lys glu val thr ser his phe gln **met** thr

901 CTC AAC GAC ATT CAG CTG CAG ATG GAG CAG CAC AAC  
leu asn asp ile gln leu gln met glu gln his asn

937 GAG CGC AAC TCC AAG CTG CGC CAG GAG AAC ATG GAG  
glu arg asn ser lys leu arg gln glu asn met glu

973 CTG GCC GAG CGG CTC AAG AAG CTG ATT GAG CAG TAC  
leu ala glu arg leu lys lys leu ile glu gln tyr

1009 GAG CTG CGA GAA GAG CAC ATC GAC AAA GTC TTC AAA  
glu leu arg glu glu his ile asp lys val phe lys

Fig. 14 (continued)

1045 CAC AAG GAT CTG CAG CAG CAG CTG GTG GAC GCC AAG  
his lys asp leu gln gln gln leu val asp ala lys

1081 CTC CAG CAG GCC CAG GAG ATG CTG AAG GAG GCA GAG  
leu gln gln ala gln glu met leu lys glu ala glu

1117 GAG CGG CAC CAG CGG GAG AAG GAC TTT CTC CTG AAG  
glu arg his gln arg glu lys asp phe leu leu lys

1153 GAG GCC GTG GAG TCC CAG AGG ATG TGC GAG CTG ATG  
glu ala val glu ser gln arg met cys glu leu met

1189 AAG CAA CAG GAG ACC CAC CTG AAG CAG CAG CTT GCC  
lys gln gln glu thr his leu lys gln gln leu ala

1225 CTA TAC ACA GAG AAG TTT GAG GAG TTC CAG AAC ACT  
leu tyr thr glu lys phe glu glu phe gln asn thr

1261 CTT TCC AAA AGC AGC GAG GTG TTC ACC ACA TTC AAA  
leu ser lys ser ser glu val phe thr thr phe lys

1297 CAG GAA ATG GAA AAG ATG ACA AAG AAG ATC AAG AAG  
gln glu met glu lys met thr lys lys ile lys lys

1333 CTG GAG AAA GAG ACC ACC ATG TAC CGT TCC CGG TGG  
leu glu lys glu thr thr met tyr arg ser arg trp

1369 GAG AGC AGC AAC AAG GCC CTG CTT GAG ATG GCT GAG  
glu ser ser asn lys ala leu leu glu met ala glu

1405 GAG AAA ACA CTC CGG GAC AAA GAG CTG GAA GGC CTG  
glu lys thr leu arg asp lys glu leu glu gly leu

1441 CAG GTG AAA ATC CAG CGG CTG GAG AAG CTG TGC CGG  
gln val lys ile gln arg leu glu lys leu cys arg

1477 GCA CTG CAG ACA GAG CGC AAT GAC CTG AAC AAG AGG  
ala leu gln thr glu arg asn asp leu asn lys arg

1513 GTG CAG GAC CTG AGT GCC GGT GGC CAG GGC CCC GTC  
val gln asp leu ser ala gly gly gln gly pro val



NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
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Fig. 14 (continued)

1549 TCC GAC AGC GGT CCT GAG CGG AGG CCA GAG CCC GCC  
**ser** asp ser gly pro glu arg arg pro **glu pro ala**  
 1585 ACC ACC TCC AAG GAG CAG GGT GTC GAG GGC CCC GGG  
**thr thr ser lys glu gln gly val** glu gly pro gly  
 1621 GCT CAA GTA CCC AAC TCT CCA AGG GCC ACA GAC GCT  
 ala gln **val** pro **asn** ser pro arg **ala** thr **asp** ala  
 1657 TCC TGC TGC GCA GGT GCA CCC AGC ACA GAG GCA TCA  
**ser** cys **cys ala** gly ala pro ser thr glu ala ser  
 1693 GGC CAG ACA GGG CCC CAG GAG CCC ACC ACT GCC ACT  
 gly gln thr gly pro gln glu pro thr **thr** ala **thr**  
 1729 GCC TAG AGA GCT TGG TGC TGG GGT GTG CCA GGA AGG  
 ala  
 1765 GAG CAG GCA GCC CAG CCA GGC CTG GCC CAG CCC AGG  
 1801 CTC CCA TGC TAA GCA GTC CGG TGC TGA GGC CAG GAT  
 1837 GTT CTG ACC TGG CTG GCA CCT GAC CCT CTG CAG TCT  
 1873 TGG ATT TTG TGG GTC AGT TTT ACA TGC ATA TGG CAC  
 1909 ACA TGC AAG GCC TCA CAC ATT TGT GTC TCT AAG TGT  
 1945 ACT GTG GGC TTG CAT CGG GGG TGA CGA TGG ACA GAT  
 1981 GAA GCC AGC GGC TCC CTT GTG AGC TGA AGT CTT ACG  
 2017 GAG GAG ACG GCG TCT GCA CTG CCA TCG CAG TGA CCT  
 2053 GCA GGA CGA GTT CCT TGA GCT TTC CCT GCC TGC TTT  
 2089 GAG GCT GAG ACC CCT CCC GGC CCT TCA GAG CTC CTG  
 2125 ACA GGT GAT ACA CAC CCA GCC TTG ACC GCA CTT CTC  
 2161 TTG GGT AGC TGG GCT CTC CTA GCC TCC CCC AGA GGC  
 2197 GCC ATT GCT TCT CTT GAC TTG GAG AGG GGA TGC CCA  
 2233 GGC GTG GCC TTG GCA GGC ACT GGG AGC TAG TGA TTG  
 2269 GGC TGC TCT CCT GCC TCG AGC AGG GGC AGG AGT GTT  
 2305 TCT GGT GGG ATG ATG CGC TCG CTG GTC AGG AGC CCC  
 2341 GTG GGC GCT GCT TCC CCC GCC CTC TGG TGA TGC CAG  
 2377 GAC CAG GCC AGT GAT GCT TCT CAG TAG CCT TAC CAT  
 2413 TCA CAG GTG CCT CTC CAG CCC GCA CAG TGA GTG ACA  
 2449 AGA TCA TCC AAA GGA TTC CTT CTG AAG GTG TTC GTT  
 2485 TCG TTT TGT TTT GTT GCA CGT GAC GGT TTG TAT TGA  
 2521 GGA CCC TCT GAG GAA GAG GGG TGC TGT AGC AGT GGT  
 2557 CCC TGC GTG CCT GGC TCC AGT GTC CTG CCC TCC CCC  
 2593 CCC TCG CCA TGG CTC CTC GGC CGC CTT GGT GCT GAG  
 2629 GTT TCT GTT TGG TGA GAT CAG GTT GTC TGT TCA GAG

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Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS

Fig. 14 (continued)

2665 AGA AGA GGC GTC TGA TGG CTT TGC CGC CAG CTT GCC  
 2701 TGC GGG CCT CAA TCC CGG GAG GCC GCC CGG TTC CCG  
 2737 TCA CTG TTG TCC CCG TGC AGT GCG TTG CTG GTC CCC  
 2773 AGG ACC AGC TGC TCG TTT GCT GTA TGG GTC AGT TTC  
 2809 TGC TTC CTG CCC CCC ACT CCA CCT AAC TGC AAT CCT  
 2845 TGG GGT TTC CCT GGT TCT CGT CCC TGG TAC CTC TGT  
 2881 GCC CAA GAA GTA GCC TTC TTT GGG ATT CTT GTT CTG  
 2917 CCC ATG CGG GAG CTG CTG CTG TCT GAC AGG TGA GGC  
 2953 CTG AGA CTC AGC GGC TGA CAG AGC TGC AGA GCT CTG  
 2989 CAC GGT GGC TCC CGG GGC GGC CTC TGT GTG CTG CAC  
 3025 ACC GCT GCT CTG CTG GCA CTG GCC AGT CTG TGC AGA  
 3061 GCA TTT GAG TAC TGG CTC AGG AGG GAG GGC TCT GCT  
 3097 GGC CTC GAG GGA CAG CGC CAC GTC TCC AGC TGG GCT  
 3133 CAG GGA GAG CCC CAG ACT GGC TGC GTA GGG TGC TTG  
 3169 GGG TTT GCT TCT TGC AGT ATT TCT TGG AAG CTG TTT  
 3205 TGT TGT CCT GCT ATT CCT TCA TCT TCC ACA GTC CAC  
 3241 GCT CAG CCT TTA ACT TGG ATC CCT CAC ATA ACA GGG  
 3277 TTC ATG AGA CCC GCA AGT ACG CCC AAG CTA CGT ATG  
 3313 GCT GAG GCC AGC TGG CAG GTG AAT GGC ACG CCA TTG  
 3349 CTG CTG CTA ATC CCT GGC ATA TCT TTA GTT CAC CTC  
 3385 GAA ATG CCC CCG CCA CAG TGC AAG CAG TGA GTC CAC  
 3421 GTG CCA CCC TGG GCT GAA TCC CAC CCC CTG TGA GTG  
 3457 TTG CCC GAG ATT GTG TCT CTT CTG AAT GCC TTC ACT  
 3493 GGG AAT GGC CTC TGC CGC CTC CTG CTC AGG GAG GCT  
 3529 TTC CCC TTC CCT CAG CCC CTG TGC CAG ACT GAG GTA  
 3565 CAA GAA CCG CCA AGC CCA TGC AAG GTG TGG CTA GGC  
 3601 GCC AGG GTG CAG GAA GGA GGC AGG TAG CTG CCT GCA  
 3637 CCC TTG AAA GCC AAG AGG CCT ACG GTG GCC TCC ATC  
 3673 CTG GCT TGC CTC ACT TCA GCT ACC TCG CAT AGC CCA  
 3709 GGG GTG GGG CTA TTG GAT TCC AGG GTG GGG GGA TGG  
 3745 GAA GCT GCA GGG GGC AGG TGG CTC TCA CTA GGC TTC  
 3781 CCA GCT CAG GAA TGT GGG CCT CAG GTA GGG GAG AGC  
 3817 CTT TGC TCC ACT CCA CCC ATT TGC AGG CAT CTA GGC  
 3853 CAG TCT AGA TGG CGA CCC CTT CTC TTC CTC TCC ATT  
 3889 GAC CAA ATC GTA CCT GTC TCT CCA GCT GCT CGC TTG  
 3925 CTC TGC TTT CCA AAG TCA GCC CAG GTA CCC AGG TGC  
 3961 CGC CCA CAT TGG CCT GGA ACC TGG ACC AGA GGC AAG  
 3997 GGA GGT GGC CTA TCC TTG AGT GAT AGC CAG TGC CTT  
 4033 CCT CAC CCG GTG GCT TCC ATG CCT GTG ACC TCA GAT  
 4069 TTA GGA CCA AGA GCT GTG TTG GTT TCT TAC GTT GTG  
 4105 AGC TTT CCC TCC AGG GGA CCA CAG CAG GTG AGG CTC  
 4141 GGA GCC CAG AGC CCT TGG CGC CGC CAG CAG TAA CTT  
 4177 GTG TCC GGA CCT TGT CCA GCT GAG CGC TTC GTG TAT

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Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
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ATHEROSCLEROSIS

Fig. 14 (continued)

4213	GAC	TCA	GCT	TCG	TGT	GTG	AGT	CCA	GCG	GAG	TGC	GTC
4249	ACG	TGA	CCT	AGA	CTC	AGC	GGT	GTC	AGC	CGC	ACT	TTG
4285	ATT	TGT	TTG	TTT	TCC	ATG	AGG	TTT	TTG	GAC	CAT	GGG
4321	CTT	AGC	TCA	GGC	AAC	TTT	TCT	GTA	AGG	AGA	ATG	TTA
4357	ACT	TTC	TGT	AAA	GAT	GCT	TAT	TTA	ACT	AAC	GCC	TGC
4393	TTC	CCC	CAC	TCC	CAA	CCA	GGT	GGC	CAC	CGA	GAG	CTC
4429	ACC	AGG	AGG	CCA	ATA	GAG	CTG	CTC	CAG	CTC	TCC	CAT
4465	CTT	GCA	CCG	CAC	AAA	GGT	GGC	CGC	CCC	AGG	GAC	AGC
4501	CAG	GCA	CCT	GCC	TGG	GGG	AGG	GGC	TTC	TCT	TCC	TTA
4537	TGG	CCT	GGC	CAT	CTA	GAT	TGT	TTA	AAG	TTG	TGC	TGA
4573	CAG	CTT	TTT	TTG	GTT	TTT	TGG	TTT	TTG	TTT	TTG	TTT
4609	TTG	TTT	TTG	TTT	TTG	TCT	ACT	TTT	GGT	ATT	CAC	AAC
4645	AGC	CAG	GGA	CTT	GAT	TTT	GAT	GTA	TTT	TAA	GCC	ACA
4681	TTA	AAT	AAA	GAG	TCT	GTT	GCC	TTA	AAA	AAA	AAA	AAA
4717	AAA	AAA										

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS

Fig. 15

1 GAC GCC TCA GAG CGG AAC AGG GAA GTG AAT CAG GCG  
37 CCG GGT AGT GGG TTG CTG GGC TGG GCT TGC TGA GGT  
73 AGA GGC AGC GCC AAG AAG AGG CCT TTG CCG CTG GTC  
109 GGG ATT GGG ATG TCG AAG AAC ACA GTG TCG TCG GCC  
met ser lys asn thr val ser ser ala  
145 CGC TTC CGG AAG GTG GAC GTG GAT GAA TAT GAC GAG  
arg phe arg lys val asp val asp glu tyr asp glu  
181 AAC AAG TTC GTG GAC GAA GAA GAT GGG GGC GAC GGC  
asn lys phe val asp glu glu asp gly gly asp gly  
217 CAG GCC GGG CCC GAC GAG GGC GAG GTG GAC TCC TGC  
gln ala gly pro asp glu gly glu val asp ser cys  
253 CTG CGG CAA GGA AAC ATG ACA GCT GCC CTA CAG GCA  
leu arg gln gly asn met thr ala ala leu gln ala  
289 GCT CTG AAG AAC CCC CCT ATC AAC ACC AAG AGT CAG  
ala leu lys asn pro pro ile asn thr **lys** ser gln  
325 GCA GTG AAG GAC CGG GCA GGC AGC ATT GTC TTG AAG  
ala val lys asp arg ala gly ser ile val leu lys  
361 GTG CTC ATC TCT TTT AAA GCT AAT GAT ATA GAA AAG  
val leu ile ser phe lys ala **asn** asp ile glu lys  
397 GCA GTT CAA TCT CTG GAC AAG AAT GGT GTG GAT CTC  
ala val gln ser leu asp **lys** asn gly val asp leu  
433 CTA ATG AAG TAT ATT TAT AAA GGA TTT GAG AGC CCG  
leu met lys tyr ile tyr lys gly phe glu ser pro  
469 TCT GAC AAT AGC AGT GCT ATG TTA CTG CAA TGG CAT  
**ser** asp asn ser ser ala **met** leu leu gln trp his  
505 GAA AAG GCA CTT GCT GCT GGA GGA GTA GGG TCC ATT  
glu lys ala leu ala ala gly gly val gly ser ile  
541 GTT CGT GTC TTG ACT GCA AGA AAA ACT GTG TAG TCT  
val arg val leu thr ala arg lys thr val

FOOTNOTES

Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
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ATHEROSCLEROSIS

Fig. 15 (continued)

577 GGC AGG AAG TGG ATT ATC TGC CTC GGG AGT GGG AAT  
613 TGC TGG TAC AAA GAC CAA AAC AAC CAA ATG CCA CCG  
649 CTG CCC TGT GGG TAG CAT CTG TTT CTC TCA GCT TTG  
685 CCT TCT TGC TTT TTC ATA TCT GTA AAG AAA AAA ATT  
721 ACA TAT CAG TTG TCC CTT TAA TGA AAA TTG GGA TAA  
757 TAT AGA AGA AAT TGT GTT AAA ATA GAA GTG TTT CAT  
793 CCT TTC AAA ACC ATT TCA GTG ATG TTT ATA CCA ATC  
829 TGT ATA TAG TAT AAT TTA CAT TCA AGT TTT AAT TGT  
865 GCA ACT TTT AAC CCT GTT GGC TGG TTT TTG GTT CTG  
901 TTT GGT TTT GTA TTA TTT TTA ACT AAT ACT GAA AAA  
937 TTT GGT CAG AAT TTG AGG CCA GTT TCC TAG CTC ATT  
973 GCT AGT CAG GAA ATG ATA TTT ATA AAA AAT ATG AGA  
1009 GAC TGG CAG CTA TTA ACA TTG CAA AAC TGG ACC ATA  
1045 TTT CCC TTA TTT AAT AAG CAA AAT ATG TTT TTG GAA  
1081 TAA GTG GTG GGT GAA TAC CAC TGC TAA GTT ATA GCT  
1117 TTG TTT TTG CTT GCC TCC TCA TTA TCT GTA CTG TGG  
1153 GTT TAA GTA TGC TAC TTT CTC TCA GCA TCC AAT AAT  
1189 CAT GGC CCC TCA ATT TAT TTG TGG TCA CGC AGG GTT  
1225 CAG AGC AAG AAG TCT TGC TTT ATA CAA ATG TAT CCA  
1261 TAA AAT ATC AGA GCT TGT TGG GCA TGA ACA TCA AAC  
1297 TTT TGT TCC ACT AAT ATG GCT CTG TTT GGA AAA AAC  
1333 TGC AAA TCA GAA AGA ATG ATT TGC AGA AAG AAA GAA  
1369 AAA CTA TGG TGT AAT TTA AAC TCT GGG CAG CCT CTG  
1405 AAT GAA ATG CTA CTT TCT TTA GAA ATA TAA TAG CTG  
1441 CCT TAG ACA TTA TGA GGT ATA CAA CTA GTA TTT AAG  
1477 ATA CCA TTT AAT ATG CCC CGT AAA TGT CTT CAG TGT  
1513 TCT TCA GGG TAG TTG GGA TCT CAA AAG ATT TGG TTC  
1549 AGA TCC AAA CAA ATA CAC ATT CTG TGT TTT AGC TCA  
1585 GTG TTT TCT AAA AAA AGA AAC TGC CAC ACA GCA AAA  
1621 AAT TGT TTA CTT TGT TGG ACA AAC CAA ATC AGT TCT  
1657 CAA AAA ATG ACC GGT GCT TAT AAA AAG TTA TAA ATA  
1693 TCG AGT AGC TCT AAA ACA AAC CAC CTG ACC AAG AGG  
1729 GAA GTG AGC TTG TGC TTA GTA TTT ACA TTG GAT GCC  
1765 AGT TTT GTA ATC ACT GAC TTA TGT GCA AAC TGG TGC  
1801 AGA AAT TCT ATA AAC TCT TTG CTG TTT TTG ATA CCT  
1837 GCT TTT TGT TTC ATT TTG TTT TGT TTT GTA AAA ATG  
1873 ATA AAA CTT CAG AAA ATA AAA TGT CAG TGT TGA ATA  
1909 ATT AAA AAA AAA AAA AA

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
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ATHEROSCLEROSIS

Fig. 16

1 GAA GAG CGA GTA CTT GAG AAA GAA GAG GAA GAA GAT  
glu glu arg val leu glu lys glu glu glu glu **asp**

37 GAT GAT GAA GAT GAA GAT GAA GAA GAT GAT GTG TCA  
**asp asp** glu asp **glu asp glu glu** asp asp val ser

73 GAG GGC TCT GAA GTG CCC GAG AGT GAC CGT CCT GCA  
glu gly ser glu val pro glu ser asp arg pro ala

109 GGT GCC CAG CAC CAC CAG CTT AAC GGC GAG CGG GGA  
gly ala gln his his gln leu asn gly glu arg gly

145 CCT CAG AGT GCC AAG GAG AGG GTC AAG GAG TGG ACC  
pro gln **ser** ala lys glu arg **val** lys glu trp **thr**

181 CCC TGC GGA CCG CAC CAG GGC CAG GAT GAA GGG CGG  
**pro** cys gly pro his **gln** gly gln **asp** glu gly arg

217 GGG CCA GCC CCG GGC AGC GGC ACC CGC CAG GTG TTC  
gly pro ala **pro** gly ser gly thr arg gln val phe

253 TCC ATG GCA GCC ATG AAC AAG GAA GGG GGA ACA GCT  
ser met ala ala **met asn** lys glu gly gly **thr** ala

289 TCT GTT GCC ACC GGG CCA GAC TCC CCG TCC CCC GTG  
ser **val ala** thr gly pro asp ser pro ser pro val

325 CCT TTG CCC CCA GGC AAA CCA GCC CTA CCT GGG GCC  
pro leu pro pro gly lys pro ala leu pro gly ala

361 GAC GGG ACC CCC TTT GGC TGT CCT CCC GGG CGC AAA  
**asp** gly thr pro phe gly cys pro **pro** gly arg lys

397 GAG AAG CCA TCT GAT CCC GTC GAG TGG ACC GTG ATG  
glu lys pro **ser** asp pro val glu trp thr val met

433 GAT GTC GTC GAA TAT TTT ACT GAG GCT GGA TTC CCG  
**asp** val val glu tyr phe thr glu ala gly phe pro

469 GAG CAG GCG ACA GCT TTC CAA GAG CAG GAA ATT GAT  
glu gln ala thr ala phe gln glu gln glu ile asp

10033539.421704

Fig. 16 (continued)

505 GGC AAA TCT TTG CTG CTC ATG CAG CGC ACA GAT GTG  
gly lys ser leu leu leu met gln arg thr asp val

541 CTC ACC GGC CTG TCC ATC CGC CTC GGG CCA GCC CTG  
leu thr gly leu ser ile arg leu gly pro ala leu

577 AAA ATC TAC GAG CAC CAC ATC AAG GTG CTT CAG CAA  
lys ile tyr glu his his ile lys val leu gln gln

613 GGC CAC TTT GAG GAT GAT GAC CCC GAT GGC TTC TTA  
gly his phe glu asp asp asp pro **asp** gly phe leu

649 GGC TGA GCG CCC AGC CTC ACC CCT GCC CCA GCC CAT  
gly

685 TCC GGC CCC CAT CTC ACC CAA GAT CCC CCA GAG TCC

721 AGG AGC TGG ACG GGG ACA CCC TCA GCC CTC ATA ACA

757 GAT TCC AAG GAG AGG GCA CCC TCT TGT CCT TAT CTT

793 TGC CCC TTG TNT CTG TCT CAC ACA CAT CTG CTC CTC

829 AGC ACG TCG GTG TGG GGA GGG GAT TGC TCC TTA AAC

865 CCC AGG TGG CTG ACC CTC CCC ACC CAG TCC AGG ACA

901 TTT TAG GAA AAA AAA AAT GAA ATG TGG GGG GCT TCT

937 CAT CTC CCC AAG ATC CTC TTC CGT TCA GCC AGA TGT

973 TTC CTG TAT AAA TGT TTG GAT CTG CCT GTT TAT TTT

1009 GGT GGG TGG TCT TTC CTC CCT CCC CTA CCA CCC ATG

1045 CCC CCC TTC TCA GTC TGC CCC TGG CCT CCA GCC CCT

1081 AGG GGA CTA GCT GGG TTG GGG TTC CTC GGG CCT TTT

1117 CTC TCC TCC CTC TTT TCT TTC TGT TGA TTG TCG CTC

1153 CAG CTG GCT GTA TTG CTT TTT AAT ATT GCA CCG AAG

1189 GTT TTT TAA ATA AAA TTT TA

1002329.131701  
1021216252001

Fig. 17

1 CA AAA AGC AGC CCA GGA CAA CCG GAA GCA GGA CCC GAG GGA GCC  
lys ser ser pro gly gln pro glu ala gly **pro** glu gly ala

45 CAG GAG CGG CCC AGC CAG GCG GCT CCT GCA GTA GAA GCA GAA GGT  
gln **glu** arg pro **ser** gln ala ala pro ala **val** glu ala glu gly

90 CCC GGC AGC AGC CAG GCT CCT CGG AAG CCG GAG GGG GCT CAA GCC  
**pro** **gly** ser ser gln ala pro **arg** **lys** pro glu gly ala gln ala

135 AGA ACG GCT CAG TCT GGG GCC CTT CGT GAT GTC TCT GAG GAG CTG  
**arg** thr ala gln **ser** gly ala leu **arg** asp val ser glu glu leu

180 AGC CGC CAA CTG GAA GAC ATA CTG AGC ACA TAC TGT GTG GAC AAT  
ser arg gln leu glu asp ile leu ser thr tyr cys val asp asn

225 AAC CAG GGG GGC CCC GGC GAG GAT GGG GCA CAG GGT GAG CCG GCT  
asn gln gly **gly** pro gly glu asp gly **ala** gln gly glu pro **ala**

270 GAA CCC GAA GAT GCA GAG AAG TCC CGG ACC TAT GTG GCA AGG AAT  
glu pro glu asp ala glu lys ser arg **thr** tyr val ala arg asn

315 GGG GAG CCT GAA CCA ACT CCA GTA GTC TAT GGA GAG AAG GAA CCC  
gly glu pro glu pro thr pro val val **tyr** gly glu lys glu **pro**

360 TCC AAG GGG GAT CCA AAC ACA GAA GAG ATC CGG CAG AGT GAC GAG  
ser lys **gly** **asp** pro **asn** thr glu glu ile arg **gln** ser asp glu

405 GTC GGA GAC CGA GAC CAT CGA AGG CCA CAG GAG AAG AAA AAA GCC  
val gly asp arg asp his arg arg pro gln glu lys lys lys ala

450 AAG GGT TTG GGG AAG GAG ATC ACG TTG CTG ATG CAG ACA TTG AAT  
lys gly leu gly lys glu ile thr leu leu met gln thr leu asn

495 ACT CTG AGT ACC CCA GAG GAG AAG CTG GCT GCT CTG TGC AAG AAG  
thr leu ser thr pro glu glu lys leu ala ala leu cys lys lys

540 TAT GCT GAA CTG CTG GAG GAG CAC CGG AAT TCA CAG AAG CAG ATG  
tyr ala glu leu leu glu glu his arg asn ser gln lys gln met

585 AAG CTC CTA CAG AAA AAG CAG AGC CAG CTG GTG CAA GAG AAG GAC  
lys leu leu gln lys lys gln ser gln leu val gln glu lys asp

630 CAC CTG CGC GGT GAG CAC AGC AAG GCC GTC CTG GCC CGC AGC AAG  
his leu arg gly glu his ser lys ala **val** leu ala arg ser lys

675 CTT GAG AGC CTA TGC CGT GAG CTG CAG CGG CAC AAC CGC TCC CTC  
leu glu ser leu cys arg glu leu gln arg his asn arg ser leu

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Fig. 17 (continued)

720 AAG GAA GAA GGT GTG CAG CGG GCC CGG GAG GAG GAG GAG AAG CGC  
lys glu glu gly val gln arg ala arg glu glu glu glu lys arg

765 AAG GAG GTG ACC TCG CAC TTC CAG GTG ACA CTG AAT GAC ATT CAG  
lys glu val thr ser his phe gln val thr leu asn asp ile gln

810 CTG CAG ATG GAA CAG CAC AAT GAG CGC AAC TCC AAG CTG CGC CAA  
leu gln met glu gln his asn glu arg asn ser lys leu arg gln

855 GAG AAC ATG GAG CTG GCT GAG AGG CTC AAG AAG CTG ATT GAG CAG  
glu asn met glu leu ala glu arg leu lys lys leu ile glu gln

900 TAT GAG CTG CGC GAG GAG CAT ATC GAC AAA GTC TTC AAA CAC AAG  
tyr glu leu arg glu glu his ile asp lys val phe lys his lys

945 GAC CTA CAA CAG CAG CTG GTG GAT GCC AAG CTC CAG CAG GCC CAG  
asp leu gln gln gln leu val asp ala lys leu gln gln ala gln

990 GAG ATG CTA AAG GAG GCA GAA GAG CGG CAC CAG CGG GAG AAG GAT  
glu met leu lys glu ala glu glu arg his gln arg glu lys asp

1035 TTT CTC CTG AAA GAG GCA GTA GAG TCC CAG AGG ATG TGT GAG CTG  
phe leu leu lys glu ala val glu ser gln arg met cys glu leu

1080 ATG AAG CAG CAA GAG ACC CAC CTG AAG CAA CAG CTT GCC CTA TAC  
met lys gln gln glu thr his leu lys gln gln leu ala leu tyr

1125 ACA GAG AAG TTT GAG GAG TTC CAG AAC ACA CTT TCC AAA AGC AGC  
thr glu lys phe glu glu phe gln asn thr leu ser lys ser ser

1170 GAG GTA TTC ACC ACA TTC AAG CAG GAG ATG GAA AAG ATG ACT AAG  
glu val phe thr thr phe lys gln glu met glu lys met thr lys

1215 AAG ATC AAG AAG CTG GAG AAA GAA ACC ACC ATG TAC CGG TCC CGG  
lys ile lys lys leu glu lys glu thr thr met tyr arg ser arg

1260 TGG GAG AGC AGC AAC AAG GCC CTG CTT GAG ATG GCT GAG GAG AAA  
trp glu ser ser asn lys ala leu leu glu met ala glu glu lys

1305 ACA GTC CGG GAT AAA GAA CTG GAG GGC CTG CAG GTA AAA ATC CAA  
thr val arg asp lys glu leu glu gly leu gln val lys ile gln

1350 CGG CTG GAG AAG CTG TGC CGG GCA CTG CAG ACA GAG CGC AAT GAC  
arg leu glu lys leu cys arg ala leu gln thr glu arg asn asp

1395 CTG AAC AAG AGG GTA CAG GAC CTG AGT GCT GGT GGC CAG GGC TCC  
leu asn lys arg val gln asp leu ser ala gly gly gln gly ser

1440 CTC ACT GAC AGT GGC CCT GAG AGG AGG CCA GAG GGG CCT GGG GCT  
leu thr asp ser gly pro glu arg arg pro glu gly pro gly ala

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Fig. 17 (continued)

1485 CAA GCA CCC AGC TCC CCC AGG GTC ACA GAA GCG CCT TGC TAC CCA  
gln ala pro ser ser pro arg val thr glu ala pro cys tyr pro

1530 GGA GCA CCG AGC ACA GAA GCA TCA GGC CAG ACT GGG CCT CAA GAG  
gly ala pro ser thr glu ala ser gly gln thr gly pro gln glu

1575 CCC ACC TCC GCC AGG GCC TAG AGA GCC TGG TGT TGG GTC ATG CTG  
pro thr ser ala arg ala \*\*\*

1620 GGA AGG GAG CGG CAG CCC AGC CAG GCC TGG CCC ATA AAA GGC TCC  
1665 CAT GCT GAG CAG CCC ATT GCT GAA GCC AGG ATG TTC TTG ACC TGG  
1710 CTG GCA TCT GGC ACT TGC AAT TTT GGA TTT TGT GGG TCA GTT TTA  
1755 CGT ACA TAG GGC ATT TTG CAA GGC CTT GCA AAT GCA TTT ATA CCT  
1800 GTA AGT GTA CAG TGG GCT TGC ATT GGG GAT GGG GGT GTG TAC AGA  
1845 TGA AGT CAG TGG CTT GTC TGT GAG CTG AAG AGT CTT GAG AGG GGC  
1890 TGT CAT CTG TAG CTG CCA TCA CAG TGA GTT GGC AGA AGT GAC TTG  
1935 AGC ATT TCT CTG TCT GAT TTG AGG CTC AGA CCC CTC CCT GCC CTT  
1980 TCA GAG CTC AAA ACA AGT AAT ACA CCA AGG TCT TGA CTG CAT TTG  
2025 TCT TGT GAG CAG GGC TTG CTT GGT CAG CTC AGG CCC TCC TAG CTG  
2070 CTT GGA GGC TCC TTT GAT TCT CTA GAC CTG GAA AAG GTG TCC CTA  
2115 GGC AGA GCC CTG GCA GGG CGC TCA GAG CTG GGA TTT CCT GCC TGG  
2160 AAC AAG GGA CCT GGA GAA TGT TTT TGC GTG GGA TGA TGT GCT GGT  
2205 CAG GAG CCC CTT GGG CAT CGC TTC CCC TGC CCT TTG GTA GTG CCA  
2250 GGA CCA GGC CAA TGA TGC TTC TCA GTA GCC TTA TCA TTC ACA GGT  
2295 GCC TCT CTA GCC TGC ACA AAT GAT TGA CAA GAG ATC ACC CAA AGG  
2340 ATT ATT TCT GAA GGT GTT TTT TTC TTT ATT TCT TTT TCT TTT TTT  
2385 TTT TTT CTT TTT CTT TTT TTT TTG CAC ATG ACA GTG TTT GTA TTG  
2430 AGG ACC TTC CAA GGA AAA GGG ATG CTG TAC CAG TGG TGC CTG GGT  
2475 GCC TGG CCT CCA GTG TCC CAC CTC CTT CAC CAC CCC ACT TGG CTC  
2520 CTT TGC CAT CTT GAT GCT GAG GTT TCC TGT TTG GTG AGA TCA GGT  
2565 TGT TTG TGG TAA AAG AAA GGA AAG GGC TTC TGA TGG CTT TGC CAC  
2610 AAG CTT ACC TGT GGG TTT CAG TCC TGA GAG GCC ACC ACC AGT TCC  
2655 CAT CAG CAC TGT CTC CAT GCA GCA GTT GCT GGG TCC CAT GTC CAG  
2700 CTG CCT CTT TGG CTT CAT GGG TTT TTC TGC TTC CTG CCC CCA CCC  
2745 CCA CAT GTG CAA TCC TCA AGA TTT GTC CTG ATT CTA TTT CCT GGC  
2790 ACC TCC CTG CCT GTC CTT GGG GAT TCT ACT TCT TCC TGT GTG GGG  
2835 CCC ATA GCT GTT GTC TAA CAG GTA AGA AAT GAA ATT GAA CTA TTG  
2880 ACT GGG CCC CAG AAA TCC ATA AAA TGG CTG CAG ACA GTT GTT TCT  
2925 GTG TCC TGT TCT ACC CCC ACT CCA GTA CAT AAC TAC TAT GTA CTG  
2970 TGT AGA GCC ATT CTA TAT GCT GAA TGT TCT GCT GTT GCA AAC TTG  
3015 CCA GGG TAT TAG CCA GTG TTT GTG CCA AGC AGT TTT CGG GGA CAA  
3060 CAG AAT GAC TCA GAC CAA GAT GGA TAG GAT GGT TAG GGC TTT GCT  
3105 TCT TGC TGT TTT TCT TTG AAC TAG TCA TTG TCC TGC AGG TCC CTT  
3150 CAT CTT CCA TAC CTA GCC CAC TCT TTT AGC CCT TAC CTT AAA TCT  
3195 CTC AGA TAA GTT GGT TCA CAA AGA ATG TTA AGT ACT GAA TCA TGT  
3240 GTG ACT GAG ACC AGA GAT GGC AAA TGA ATG GCA CAC CAT TTC TCC  
3285 TTC TCC TGC CCC AGG GCA GGT ACC ACT GAT CTG CAT CAG AGT TGC  
3330 CTG CTA TTC TCT GGT GTA TCC TTC ACA TCT AGG TGC CCT CAA GCA  
3375 GCT GTG TGA GTG TTG AGA TCT CTG CCA TCT CTG GCT GAG ATA CTG  
3420 CTG TCC TGT GAA GTG TTT CCC ATG ACC TTT TTC TTC CCC TTT GAA  
3465 TCC CTC TTG TCT GGA GTA GTC CTT GCC TTC TTC TTG CTC CAG TAG

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Fig. 17 (continued)

3510 GCC TTT TCC TTA CCC CAG CCC TTG TGC CAG GCT AAG CTG GTA CAA  
3555 GAG CTG CCA ACT CAC AGA GTT TTG CTA GGC GAG AGA GGT GCA GGG  
3600 AAG AGG CAG AGG TAT GCA CCT TCC CCC TTG AAG AGA GGG GAA AGG  
3645 CCT ACA GTG GCC CAC ATA ATT GCC TGA CTC ACA CTT CAG CTA CCT  
3690 CTT AAT GCC TGT GGA GGG ACT GGA GCT GCT GGA TCC CAG TGT GGT  
3735 GGT GTA GGA GGC CAC AGT GAG CAG GTG GCC CCA GCT GGG TTT CCC  
3780 AGG TCA GGA ATG TGG GCC CCA GGC AAG GTG CAG CCT TTG CTC ACA  
3825 GCT CCA TCC ATG TCT AGA CCT TCA GGC CAG TCT GCA GAT GAG GTT  
3870 CCC TAC CTT TTT CTT CTC TTC ATT GAC CAA ATC AAC CAA TCA CTA  
3915 CAG CTG CTC TGC TTC TGC TTT CCA AAG TAG CCC AGG TCC TGG GCC  
3960 AGA TGC AGG GGA GGT GCC TAT CCA TGA GTG AAG GCC AGT GTC TTC  
4005 CTC ACC TGG GTG GTC CCA CAC TTG TGA CCC TCA GTT TTA GGA CCC  
4050 AAG ATC TGT GTT GGT TTC TTA GAT TGC TAG CTT TTC CTC CAG GGG  
4095 ACC ACA GCA GGT GAA GCT CAA GAG CGC ATG GCT CTG CTA ATA GTA  
4140 AAT TGT TTT CAG GGC CTT GTC CAG CTG AGA GCT TCA TGT CCA CCA  
4185 GAT TCT GAG AGG TGT CAG CAG CAC TTT TTT TTT TTA TTT GTT GTT  
4230 TGT TTT CCA TGA GGT TAT CGG ACC ATG GGC TGA GCT CAG GCA CTT  
4275 TCT GTA GGA GAC TGT TAT TTC TGT AAA GAT GGT TAT TTA ACC CTC  
4320 CTC CAC CCC ATC ACG GTG GCC CTG AGG GCT GAC CCG GAG GCC AGT  
4365 GGA GCT GCC TGG TGT CCA CGG GGG AGG GCC AAG GCC TGC TGA GCT  
4410 GAT TCT CCA GCT GCT GCC CCA GCC TTT CCG CCT TGC ACA GCA CAG  
4455 AGG TGG TCA CCC CAG GGA CAG CCA GGC ACC TGC TCC TCT TGC CCT  
4500 TCC TGG GGG AAA GGA GCT GCC TTC TGT CCC TGT AAC TGC TTT CCT  
4545 TAT GGC CCA ACC CGG CCA CTC AGA CTT GTT TGA AGC TGC ACT GGC  
4590 AGC TTT TTT GTC TCC TTT GGG TAT TCA CAA CAG CCA GGG ACT TGA  
4635 TTT TGA TGT ATT TTA AAC CAC ATT AAA TAA AGA GTC TGT TGC CTT  
4680 AAA AAA AAA AAA AAA AAA

FOIA b 7 - Exempt

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ATHEROSCLEROSIS

Fig. 18

GTG GAC GTG GAT GAG TAC GAC GAG AAC AAG TTC GTG  
val asp val asp glu tyr asp glu asn lys phe val

GAC GAG GAA GAC GGC GGC GAC GGC  
asp glu glu asp gly gly asp gly

1003937

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NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS

Fig. 19

	1		50
Rabbit	MSKNTVSSAR FRKVDVDEYD ENKFVDEEDG GDGQAGPDEG		EVDSCLRQGN
Human	.....		.....
	51		100
Rabbit	MTAALQAALK NPPINTRSQA VKDRAGSIVL KVLISFKAGD		IEKAVQSLDR
Human	.....K...		.....N.....K
	101		150
Rabbit	NGVDLLMKYI YKGFESPSDN SSAVLLQWHE KALAAGGVGS		IVRVL TARKT
Human	.....		...M.....
	151		
Rabbit	V		
Human	.		

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Fig. 20

	1		50
Rabbit	EERVLEKEEE EEEEEDEDED DDDVVSEGSE VPESDRPAGA QHHQLNGGER		
Human	..... .DDD..EDEE ..--.....		
	51		100
Rabbit	GPQTAKERAK EWSLCGPHPG QEEGRGPAAG SGTRQVFSMA ALSKEGGSAS		
Human	...S....V. ..TP....Q. .D.....P. .... .MN....T..		
	101		150
Rabbit	STTGPDSPSP VPLPPGKPAL PGADGTPFGC PAGRKEKPAD PVEWTVMDVV		
Human	VA..... .P.....S. ....		
	151		200
Rabbit	EYFTEAGFPE QATAFQEQEI DGKSLLLMQR TDVLTGLSIR LGPALKIYEH		
Human	.....		
	201	220	
Rabbit	HIKVLQQGHF EDDDPEGFLG		
Human	.....D....		

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fig. 21

	1		50
Rabbit	MKNQDKKNGA AKQPNPKSSP GQPEAGAEGA QGRPGRPAPA REAEG-ASSQ		
Human	-----	-----P... .E..SQA... V....PG...	
	51		100
Rabbit	APGRPEGAQA KTAQPGALCD VSEELSRQLE DILSTYCVDN NQGAPGEDGV		
Human	..RK..... R...S...R. ....	.....G.....A	
	101		150
Rabbit	QGEPPEPEDA EKSRAYVARN GEPEPGTPVV NGEKETSKE PGTEEIRTS		
Human	....A..... .T..... -.... Y....P..GD .N.....Q..		
	151		200
Rabbit	EVGDRDHRRP QEKKKAKGLG KEITLLMQL NTLSTPEEKL AALCKKYAEL		
Human	.....	.....	
	201		250
Rabbit	LEEHRNSQKQ MKLLQKKQSQ LVQEKDHLRG EHSKAILARS KLESICRELQ		
Human	.....	.....V.....	
	251		300
Rabbit	RHNRSLKEEG VQRAREEEEEK RKEVTSHFQM TLNDIQLQME QHNERNSKLR		
Human	.....	.....V.....	
	301		350
Rabbit	QENMELAERL KKLIEQYELR EEHIDKVFKH KDLQQQLVDA KLQQAQEMLK		
Human	.....	.....	
	351		400
Rabbit	EAEERHQREK DFLLKEAVES QRMCELMKQQ ETHLKQQLAL YTEKFEEFQN		
Human	.....	.....	
	401		450
Rabbit	TLKSSEVFT TFKQEMEKMT KKIKKLEKET TMYRSRWESS NKALLEMAEE		
Human	.....	.....	
	451		500
Rabbit	KTLRDKELEG LQVKIQRLEK LCRALQTERN DLNKRVDLS AGGQGPVSDS		
Human	..V.....	.....SLT..	
	501		550
Rabbit	GPERRPEPAT TSKEQGVEGP GAQVPNSPRA TDASCCAGAP STEASGQTGP		
Human	.....	...A.S...V .E.P.YP... ..	
	551		
Rabbit	QEPTTATA		
Human	....S.R.		

FOOTNOTES

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Fig. 22 (1/5)

1 AAGCTTTATAAGATTTAACTACCTAATAAGGTAGAGAAGTAATTTATGTGCCCACTAAA 60  
61 AAATACTCAATTTCTGAATGTTTCGTCCTCCAAAATTAAGTTGTCAGATCATTAAATCATTGAC 120  
121 TAGAAACACGTTGAGTACCTATTATGTACTAGGCACTTAGATCATTGTGAGACAATAAAA 180  
181 AATACTGCATTAGAAAAGGACATTTTTTCACATCTTAAATGCAATAAGCATTATTTGGCTG 240  
241 GCAGTTAATTACATTTAACACATTAAACATATAGAGCAAAATTCTGAGCAATCAAAATAA 300  
301 TTATACCCTTGAGCAATCGATTATTTAAATTTCTTCACTATTCCCTTAAGCTGATTTCT 360  
361 ACTCTGGGATTCTTTCATAGTTCTCAAATAAGAAAATAAAAAATTTCTAAATAAGGCAA 420  
421 TACAAAAGAATAGAAATGTAAGAGAAGAGATATATTAGCTCTTGAATCCCTGTTTCCATT 480  
481 TGCTGTCAATAGTGCCTCTAATGTTTCGATTTTCTCTTCAAAGAAAAATCTTGATTTAAA 540  
541 GGAAGAAAAAGTACAATCACCTTTAACAGCTAAAGTATACTGATTAGCATCTACTAAAGT 600  
601 TAGCAAAGACTGAACTGAAAAAAATTTGTAATCTTTATTCTAAGTTATATAACGCCA 660  
661 TTCACCATAGTAATGATTTTATACTTTGGTATATGGCTTTTTTAAAATAAATATTGCCAAC 720  
721 AGGTAAAAATTTTCTTTGCTGTCTTAAGGCATTCTTAAGAGAATTTTACCAGTGTGT 780  
781 GTTCATAACTTGAATGTTAATTTAAACAATGTTACTTCTATCACCTAAATGATATACTTA 840  
841 TAGAAGAGTGGTTTAAATGGGAACAGAAAAACACCACATTGCTTCTTCCCAAGAAAAAGG 900  
901 GATGTATTCCATTCTCGAGGTCTCTCTCCCACTCTCTATTTATATATAATATACTGCATA 960  
961 GATAAATATACACACATTATATATGATTTTTTTGAAGTAAAGAAGACTGGACATATGT 1020  
1021 ATTTACATGTATATATCCAAATAATTTAATTTTGAGATCTCTCTCCCTCTTCTGATTT 1080  
1081 ATTATTCTCAGTATGAATTTCTCAAACGTGTACGGTCTTTTACATTTTCAATTCATTCAAG 1140  
1141 CATGTATCGAGTCCCTTCTGCATGCTTAGCTTTTTTGTATATGGAAGGAAGATACAAAAG 1200  
1201 AAAAAGTGTCTGCTTCCAGATCTTCCATCTCTTCTAGGAAGGAGATAAAACACCA 1260  
1261 TATATCATTAAGAAATTTATAAGACTAGTCCCAAAACCAATGGTACAAGCAACATGCATT 1320  
1321 TTACATTTATGTAGAATTTTAGAGCTTGGAAACACTTTCGTGATATATAATCCTAAGAAC 1380  
1381 AATCTTGTAAGTGCACATTATTAGCTCCATTTCAGTGATGAGGAATCTGAGACAGAATT 1440  
1441 TTAAGTGACATGTCTCGTTCAAACATTATGAGTGAAGAGTCAACACTTAAGCCTGAGTT 1500  
1501 TTCTGATTCTAAGCCTAGTGCTCTTTTCAACACAGCACTGGAAACCAAGATTGTGGTAC 1560  
1561 ACAACAAGGCAACAGCCAGTCTTCTGCTGAGGTCCAAGTAAAGTGGACCCATACCGAG 1620  
1621 CAGTGTCCAGCCAAATGTCCAAATTAATTTTATCCTGCAATATTTGTTCTTCAGTGTA 1680  
1681 TACACACAGCACAACTACCATTTCTTTCGTCTTAGTGCTTTTATCTCCTACATTCCAGAA 1740  
1741 ATGGGGATGTCAAATATTTTTTAAATCTGGCCTAGATGGAATCATATAAATCTCAAATC 1800  
1801 ATAATATAAATCTTAAAGTCTGGTTTCCACCAATCCTTCCACATTTTGTTCCTCCCCAG 1860  
1861 CACTAGAGAGCCCTAACCTACCCTCACCCCTTTCGAGCATTCTTGCTCCAAACGACCACCT 1920  
1921 ATTTTAAAGATGTCAATGACCTTTCCCAAATCTACAAATTCACCCAGTTTGGCCACCC 1980  
1981 GACCCAGCGCCTGCCCGGACAGTTCCCTCCCTCCCAATAGATTTGATACCGAGTTCA 2040  
2041 GGTTCTGCAGATCCCGTTGCGATGCTGTACACAGCACTGACAGATAAGATTTGACCTTT 2100  
2101 CGACTCCGTCCTTGGGGACTTCCCGCTGGCCAAGAAGGTAGTTCCAATCCAGGAACCG 2160  
2161 GGCTTCTGCTCAGGAACGCAGCCTCTAGCAGCGCACAGTCTGAGGCAATGTCTCCGGCA 2220  
2221 ATTAGAACGATGCTGGGCGCCCGGGTGTGCATCACTCTGCCTCATACTCCTACCAACTGC 2280  
2281 AGGGCACTCGGTCCGGCAGCCAGTCCATCCCACCCACACCAAGTCCAGCCAGCCGGAC 2340  
2341 CTTACGCAGGACCCCGATGATAGGTCGTTGACGGCTGCAGCAAAAGCCAAGGCCACCTGC 2400  
2401 CGCTGCTGCCCATCCCCGCCAATCTGAGACCCCTAGACTGGACCGCAGAAAAGCGTTTC 2460  
2461 TATGGGAACCCCCCACCAGAAATCACGTGACGCAATCGGACGACCAATCGCTTCTTACC 2520  
2521 TCTGCCCCGCGTCCAGCTTTTGGCCCTCCCTCTCGCCCCGCGCTCCTTCGCCCAGCCCCG 2580  
2581 CCCCTTGCCTGCGGAGAGCCCGCGCTGCGCGCTGTGTCTGCGCGCTCCTTCCCTCGCG 2640  
2641 CGCGCTCTCCGTGGAAGAGCAGGGGCAGCGTGGGAGGCGCAAGGGAGCGCGAACCTGAG 2700  
2701 GAGGAAGAAACGGGGCTAGCGCGCAGGCCAGAACGGTCCGAGCCGCGCGAGTCGGCGAC 2760  
2761 GCCTCAGAGCGGAAGAGGGAAGTGAATCAGGCGCCGGGTAGTGGGTTGCTGGGCTGGGCT 2820  
  
2821 TGCTGAGGTAGAGGCAGCGCCAAGAAGAGGCCTTTGCCGCTGGTCCGGATTGGGATGTCTG 2880  
M S  
  
2881 AAGAACACAGTGTGCTCGGCCCGCTTCCGGAAGGTGGACGTGGATGAATATGACGAGAAC 2940  
K N T V S S A R F R K V D V D E Y D E N



--- -- fig. 22 (continued; 2/5) ---

2941 AAGTTCGTGGACGAAGAAGATGGGGGCGACGCCAGGCCGGGGCCCGACGAGGGCGAGGTG 3000  
K F V D E E D G G D G Q A G P D E G E V

3001 GACTCCTGCCTGCGGCAATATCCTTGCATTACCGCCCTCCCCACCCAGCCCAGCCCAG 3060  
D S C L R Q

3061 CCCGCCCTTCTCCTGGGACCCGGGAGCCTGCAGGATCCGCGGGGCACCGGCGCGGAGCTG 3120  
3121 CCTCTCAACCTGCGGCTTAACCTGTCTCTTTGGGATCGCCCGCTCTGAGAGGGCAAGGGG 3180  
3181 GAAGCCCCCGTTTCTACCCAGTCGGCAGGAGACGCGAGGGTCCCCTCTTGAAGCCTG 3240  
3241 CCCTACCCCGCGCGCCTTCCACGCCCCCAGATTCTCAGGTTGCACCCGAGTGCCTGCCT 3300  
3301 GCCTCGGGAACCTGGTCCCGCCGCGCCCGCCCTCGCGGCGCTGGGGAAGGCGGCCCGGCT 3360  
3361 GGTGGGGAAGGCTGGTGCCGACCGCCTTAGTTTTCTTCCTAGAACTCTGATTTCTGCG 3420  
3421 GTCACATTAGCTCCAGAAATTTCTGATTGTGGGGAACCTGCATCTTTCTTAGTGTTTT 3480  
3481 GTTTTTTGGTTGTGTTTTTGTATTGGTAGCGTTAAGGTAGTTTATTGCTTACCGGGGG 3540  
3541 CCGGGGGAGATGGGACTGTTTCGAAAATTGAGGGTCCCTGTGCTTTCAGCCCATTGGCCTT 3600  
3601 TTTAAAAAAGAGAAAGAAAG 3660  
3661 AATTTGTAACTGGGGGAGGGGAATGAATACAAAAATACAAAACTCCTAGAAGGAAGCT 3720  
3721 TGGAGCCTTTTACCTGCTAAGAAAAGGACAATAGAAAAACAACGGGGAATGCGTGTGGA 3780  
3781 GAATCCTTGGAAATATTTAAAAAATACCCCAATGAATAAGATAGAAGATGAGTCATTCTG 3840  
3841 ATAAAGCAGAATCATTTTTGTAACTCCTAAAATTCTTTCCATTTTAGTTAAATATGGCAG 3900  
3901 TCAGTTCCCGGTTTCTGTTTTTGCATATTTGAATATTTCATAACTTTGGCTTCGATTTGC 3960  
3961 ATTACATCTTTTTTAGAAAAATGTAATGTTGCAAAAAAACCGAAGCTGTAGTTTATGAA 4020  
4021 AATCTCAGACACTGAATTTGTATGCATTTCTAATTCTTGGGTGTATTTCATAAGGAAGACT 4080  
4081 CTCAACAATGTCCTGTTATAGTGGGGAAATATGAGAGTGAAAATATTTAATGGCAACAAT 4140  
4141 ATCCTTTTTTAAAGGCACCTAAATAGAGCATTAGACATTTATCAATATATAGATAGTGCT 4200  
4201 TTGCCCAACTTTTACAATTAATTAGCTGTGCTCTTTGCATTATTTAAATACTTAAGTG 4260  
4261 CTTGGAGTTATAAAAAATGAGCTAATCTACATCAGGCATGCTTCTCTAGAAATCCCTGCA 4320  
4321 GCCTTGAAAATAACAGCTTGTCAACCAGAGATTTTGTGTAAGAACTTTTCTTTAGAAAA 4380  
4381 TAAATGGTGAACATGCTTCCATAAAACATTATTTGTGATGGGATAAGATGGTGTGTTTATG 4440  
4441 AAACCCAGTGATTTTTAGGTAATTTGTGGTGACTTTTAAAAGGTACTGCTGTATCCATA 4500  
4501 TCAGTGGATCTGCTTTTTGATCAGTTTCTTAAAAATATAAAGATACTGTCTCTTCTTAC 4560  
4561 CGTTACATACAGCCAGGAAAGACAGCCCTAGTGGTGGGGTACTAGAGTTGGAGGAACAAG 4620  
4621 TGAATCTGTGGTTTTCCTTTTAGGGGAATGTTGTACATTCTGACAGTCTGATTGGCCT 4680  
4681 TCTGTTTCTCATGCTTGCTAACTCACTAGTGCTTTCAAAGAGAGCCTGAATTTAATAGGT 4740  
4741 ATGGTCTAACACAGTTTGAATAACCTTTGTGAAATATGAGAGAAAATATCTAAAGCAAAA 4800  
4801 AATTAAGCTGCCACCTAAGGGACATATGAATTATTACATCTTCTGTGATGCCTCTTTTCA 4860  
4861 TCAATATTGAGAGATTGCTAATGTGTATCATTGAGATTGCTAATCTGCCAGCATGTTCTA 4920  
4921 CCAGCATTTAGATAATACAGAATATGGTTCTAGCAAAAAGTTTGGTCTTTATTTTTTCAA 4980  
4981 TTAGAATCACAGGAAAAGACATATTTGGTTGATAATAGGTTATTTTCAATTTGGGGGACTA 5040  
5041 ATAATTCTGATATATATTTTAGGATTTCTTTAACACCACTCTAGGTAATGTTTGCATATG 5100  
5101 TATCTACTGGGAAATGAAAGACTATCAAGGTGTTCACTTGATAGTTAGAACCAAGGGTG 5160  
5161 AAACAGTCTTTGCTTTATTAAGAAAAAGTCTAATGTTCTATTTTGCTTTTGATATTTTGC 5220  
5221 CTTTGATTAACATCCTGGAAACCAACACATTGAATTTCCAGTATTGAACATAGTGACCAA 5280  
5281 AGTAATTTTCTTTTTATATGTAAATCAAGTCATAAAGAACCAGTGTTTATAATGCTTTCT 5340

5341 GGGGGCCATCCTTTGCTGTTACACCCTTAACTTCCATCACAGGAAACATGACAGCTGCCC 5400  
G N M T A A L

5401 TACAGGCAGCTCTGAAGAACCCCCCTATCAACACCAAGAGTCAGGCAGTGAAGGTGAGTC 5460  
Q A A L K N P P I N T K S Q A V K

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- - - fig. 22 (continued, 3/5) - - -

5461 GCAGACTACAACACAGTGATCTCTGCTGATATCTTATTCTTAGTAAAATCCTTGCAGTGC 5520  
 5521 AAAAAAAAAATCAATATTTTAACTGTTTGCTATCTTTGACAAGAAGAGTTTATAATGTAGT 5580  
 5581 TTGATAGGTAAAAATTTACGTGAAAAATAGCCCTATAATGTAGTTATGATAATGCTGC 5640  
 5641 ATGGTAAGATACAGTAAGTTCAAACGATAGTGAATCATTTGTGTGTGTTTTTAGAGGAG 5700  
 5701 ACCACTCAGGCTGAATTTGAGCAAAGGTTGAAAAATAAGTTAAACCTTTACAAAAATAA 5760  
 5761 ACAGATTGTAATTGCTTTTTAAAGATTTTTTAAACCATACAAATACTAAATACTTATTA 5820  
 5821 TAGAAAGCTCAGACATATGAGAAGGTTAAAAAGATAGTGGTTTGTGGTCCCAGCACCCAG 5880  
 5881 AGATAACAGTTACTACTTTGGGGCCTTGCTGTATTGTTACAGAGTTCCCTTTTGTTTTTT 5940  
 5941 TAAGAATGAATTTTTTAAACGGGCTTTTTCAGCTATATGCAATGGTACATGAGCTTTCCT 6000  
 6001 TCCCCAATAAGTTAATAGCCTTTTTTAACTTGTATATGGATAAGCTCCAGTGTATACA 6060  
 6061 TAACTAATCTTTTGTATATTTAGACTGACTTTTTTTTTTCTATTGTAAACCACTGAAA 6120  
 6121 TCAATATTTTTTGGTAAATTTTAAATTGTTCTCTTTGAGTAAATTGCTAGCAGTGAATTA 6180  
 6181 CTGGATCAAAGAATGCACTTTTTTTAAGGCTTTTGGTATGCAGTATTGCCAAATTGCC 6240  
 6241 TTCAGAACAGTTGTGCAACTTACATTCTCTGCAGTCTTTACTAATTCTTAACCTATTTA 6300  
 6301 CGTATTTATTTAAATGATGCCCATAGCATCAACCCCGTTGTCCATAGCTATTCATACAT 6360  
 6361 CCTAGGAGCTTCAAGAATCTCAATTGAATAGTAGTAAGTAATAACTTAGGTAAATGCATA 6420  
 6421 ATAATTATCTCGTTAACATAATTTTTTATTGGGGAAAATTTCTTTGGTTTTTACAAGTTG 6480  
 6481 TAAAGATTGTCTGTTGAAATTTCATTTTTACCCTGGATGCAAGATATTTTTCTAAATCTG 6540  
 6541 GTAATTGCAGTCTTTTAAACCAAAGATAACAGTAGGTGGTAGAAACATTCTGTGAATCCT 6600  
 6601 GACCAGTAGGAATGCTGGAGGTATCACTTTGTGTTGAATGGAAGGAGAAACGAATTGTTG 6660  
 6661 AAAAGGTCAGTTAAGTGTTTCTTTGCTTGGCCGGATGGGTAAAGAAAATAACTGCTTTTG 6720  
 6721 AAGCAGGCTTTTGCCAAAGAAAAAGATCATTATTAATGAACATCACTATATTTTCATATC 6780  
 6781 TACAGTCAATTCATATAAATTACAGTCAATTTTCTTTTAAAGACAGCTTGGTTTATTAAAA 6840  
 6841 TTTTTAAATAAAAAAGTTTTTAAAGAAAAATTACTTCTGAAGGATAATTCAAGGTGAAC 6900  
 6901 TGCAAATCTGCCTCCTTGTGTTTGGGAATTTTTTTTTTTTTTTTTTTTTTGGAGACG 6960  
 6961 GAGTCTCACTCTATCACCCAGGTTGGAGTGCAGTGGTGAATCTCAACTCACTGCACCCT 7020  
 7021 CCGCCTCCCGGGTTTAAAGCAATCCTCCTGCTTCAGCCTCCCGAGTAGCTGGGATCACAGG 7080  
 7081 CACACACCACCATGCCTGGATAATTTCTGTATTTTTAGAAGAAAACAGGGTTTTACCATT 7140  
 7141 TTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGATCTGCCCATCTCGGCCTCCCAA 7200  
 7201 GTGCTGGGATTACAGCTGTGGGCCACCAACCCCGCCGTTTTGTTGGGATTTTTTTTTTT 7260  
 7261 TAAGATCAAGACATAAATTTAAATGTTGTTTTAATAAATTGTTAAATTATCACATTGATC 7320  
 7321 TGTTAGCAAATCCTCTCAGCTCTGCCTTCAATTATGTTAATAGTCTGTCAAGTTTCTTAC 7380  
 7381 CACCTCCACTGCTACTATGCTTACCACATCCAGCCTGTATTATTGCAATTGCCTCCTAAT 7440  
 7441 TGCTCTCCCTGCTTCTACCTTATCCCTACTCCACAGCTTATTTTCTGTAACATAGATG 7500  
 7501 CCAAAGCAATCCTGTTAAATGTGAGTCAGATTATGGCACTGCTTTAAACCTTCCAAT 7560  
 7561 GTCTTCTCATTTCTCTCAGTAAAAGCCAAAGTCTTACAATGCCTGTAGGCCTTACACGA 7620  
 7621 TCTGTCTCCCATAACTCTGACTTACTCACGTGCTTTTCTCCCAATCCACTCCAAC 7680  
 7681 CACATTGGGTTTTTTTTCTGTTCTCGGAACACACTGAACACACACTAATAGCACTGTTCTT 7740  
 7741 TCCTCTGTCTGAAACACTTTCCTCAGTTATCCCAAGCCTTCTTTCAGTCCTTCAGGTCC 7800  
 7801 TTAATCAAATGTCACATTCATAGTGTAGACTTCTGAAATTCTAAACCCTCCTCATACAG 7860  
  
 7861 ATATGTCTAAATGTTCTGTTATTTATTGACCCACCAGGACCGGGCAGGCAGCATTGTCTT 7920  
 D R A G S I V L  
  
 7921 GAAGGTGCTCATCTCTTTTAAAGCTAATGATATAGAAAAGGCAGTTCAATCTCTGGACAA 7980  
 K V L I S F K A N D I E K A V Q S L D K  
  
 7981 GAATGGTGTGGATCTCCTAATGAAGTATATTTATAAAGGATTTGAGAGCCCGTCTGACAA 8040  
 N G V D L L M K Y I Y K G F E S P S D N  
  
 8041 TAGCAGTGCTATGTTACTGCAATGGCATGAAAAGGTAAGTTATGAATTATAAATCTATAT 8100  
 S S A M L L Q W H E K

1003593 431001 666001

Applicant(s): Ann M. Lees et al.

NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS  
AND THEIR USE IN DIAGNOSING AND TREATING  
ATHEROSCLEROSIS

Fig. 22 (continued, 4/5)---

8101 GACTGGTTCTTTTACAATAGGGAATGACAATGACAACCTCTCTCACCTAAATAACCATTT 8160  
 8161 TGATTTGTTGTACATTTTGTATTACAAATAAAATGCATGAAAAGGATAGTTCATATTT 8220  
 8221 ATGTTTACTAGCCTTGGTCTTAAGAGATTCTGATTCCAACACTTGTGTTTATTCAACAAT 8280  
 8281 GATTATTAGTAATTAACATAATCTTGAACCTCTGAATTAAATCAAACTTTGTAAAAGAA 8340  
 8341 AATAAGCAATACAAATCAAGAATTCTTTCACAGTGACCAAAGGTGAAAACAACACAAGG 8400  
 8401 ATCGAATATGATTCAACCA 8419  
 8420 TTAAAAGGAATGACATTCTGACACATGCTATAACATTAATAAACCTTGAAAACATACCAA 8479  
 8480 GTGAAATGAGCCAAACACAAAAGAACTAATATTTTATAATTTTACTTATATGAAATAATC 8539  
 8540 TAGGATAGGCAAACACAAAGGGACAGAAAGTCCTTAGAGGTTACTAGGAAGTAGGGAAAG 8599  
 8600 CAAGGAATAGGGAGTTAGTGCTTAATAGGTACAGAGTTCCTCCTTGGAGTGGTAAAAAAG 8659  
 8660 TTTTGGAAACAGATAGTGGTGATGGCTACAGTACATTGTGAATATAATTAATGCCAATGG 8719  
 8720 ATTTTACACTTAAAGATGGTTAAATGGCAAATTTTGTGTTAGATATTTTACAACCTTTTT 8779  
 8780 TAAAGAATTAGGAGTTTGGAGGATCAAGAATTCTTAAATCATGTTTTTCTATTTTCATGT 8839  
 8840 GTATATTTTGAATGTAAGTAGATGCTGGTACATCATCTGTCAAAGAGTATAAGTGATT 8899  
 8900 TTGAGCTTTGGGTAAAAACTGGATAACATGTAAATAGAACCAGTCATAAAAATATTGAG 8959  
 8960 TGTTTGAAGTGATCTGAGTGAAAACACAAACATAAGAAAAAGCACATAGTAAACAAT 9019  
 9020 AGTTCCCCCTTTTACTCTAAAATGCACCAATTTGGGTAGTAATTTATATGGCACCCTATT 9079  
 9080 CATGGAACACTTTTCTGTTGCCAGGTACCATACTAATTAATGTTTTTATTTAACCTTTACAAC 9139  
 9140 AACCTGTGGAGTATATAAATATCTTTATCATCTCAATTTACAGATGAAAAGCTAGCT 9199  
 9200 TTAAAACCCAGCCAGCGTAGTTCTAGCATAGCCTCAAGATTGCAGTGAACATTGATTAC 9259  
 9260 TTATTATATTCCACATATTCTTCAAAGGACTTTATAAATATTAACCTATTTAATCCTCAT 9319  
 9320 AAAAAATGGAGGAAATGCTTGCTATTATTCTCTTTTGTCACTGAGGAACTGAGGCATG 9379  
 9380 TGTGAAGTCTTCATTCTTCCAAATGTCAGTCACCAGTTTTTTACCAATCTTCGAAGTATT 9439  
 9440 TCTGAAATCTATCTGTTCAAGCGTATCTAATGCAGCTGTTTCACAGCATCTCTCCAGTCT 9499  
 9500 GTTGCCATAGCTTCTGACTGGTTTTCCAGTTAACAGTTTTGCCTCCTTCAAATCTGTTT 9559  
 9560 TCCACCCAGCCATCAAAATGATATCTTTAAATCAAAATTGCCCTTGTCAAGTCACTGCA 9619  
 9620 GGGATAAAGTCAAAGTTCCCAAGTCTAGCTTCATCTTCCATGTCATTCTTCCCCTCAGGC 9679  
 9680 TATAGCAATGCCAGCCTTTTTCTCTGAATGCACCATATTGTTTCACACCTCCATACATTTG 9739  
 9740 CTCATGATTTTCTGGTGTTAGCCTGTACCTACTCATTCTTTTTAATGTGTCAATTTCTCTC 9799  
 9800 ATGAAGCCTTAGCTGAAACATTCTCTATACTGTTAATCTGGGTATAAGCCTCTCCCTGG 9859  
 9860 TGCTTTAATAGCACCTGCAGCACAACTCTCATTTTCATACATTAGATTAAATTTACCTGTT 9919  
 9920 TATATGTCTGTCTCTCATGCTAGACCAGAAAATGCTGTATTTGTTCACTTTTGTATCCC 9979  
 9980 CAGCATCTAGCACAGTACTCAGTATACAAAGGTATTCCATAAATATTTTTTGAACAGAAA 10039  
 10040 GAAACCAGAGCTCAGATTCTCTAATACTTGATCATTAATCTCTATTTTCAAATTAGAGTC 10099  
 10100 AGAGTTAAAGTTTCTAAGTTCTTAGCTATTAAACAATACCTTCTTTCTTTGGGAGAAAA 10159  
 10160 AAATCTGACAAAGGCTGACTAATCGAAGTGGAAGTTGGGATGGTTGATCCAGTTTGAAT 10219  
 10220 TTTCTTCTGACTATGTGGTGAGAATGAGAAATGCAGAATGTCCACCTGTTTTGAGCAGGA 10279  
 10280 ACACTATGCTGCAGATTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTGTAGACGGAGTCTTGC 10339  
 10340 TCTGTGCGCCAGGCTGGAGTGCAGTGGCGCAATCTCGGCTCACTGCAAGCTCCGCCTCCT 10399  
 10400 GGGTTCACACCATTGTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCACCCGCCA 10459  
 10460 CCACGCCCGCTAATTTTTTTGTATTTTTTAGTAGAGACGGGGTTTACCATGTTAGCCAGG 10519  
 10520 ATGGTCTTGATCTCTGACCTCGTGATCCGCCGGCCTCGGCCTCCCAAAGTGCTGGGATT 10579  
 10580 ACAGGCGTGAGCCACCGCGCCCGGCCTATGCTGCAGATTTTTTAAACATTATTTAGAAT 10639  
 10640 TAATGTACTAAAAATGTAACTAGTATCTCACTAGAATGTAACCTCATGAGGGCAGGGACT 10699  
 10700 TTCAAGGTTTTGTTTATTACTGTAACCTCAGTGCCAAGAACAGTACCTGGTGCATAATTG 10759  
 10760 GTGCTCAAGAATTTATTATTTGTTAACTAATAAATTACAGGCTCTATAGCAGTGCCCATTC 10819  
 10820 CTTCTTTAAGAAAAATGTTTTACCAAATATGAGAATTGACCTTTTATTATTCTGTCAACA 10879  
  
 10880 TTTACATCCTGGTTTTGTTTTTAGGCACTTGCTGCTGGAGGAGTAGGGTCCATTGTTTCGTG 10939  
 A L A A G G V G S I V R V  
 10940 TCTTGACTGCAAGAAAACTGTGTAGTCTGGCAGGAAGTGATTATCTGCCTCGGGAGTG 10999  
 L T A R K T V \*

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Applicant(s): Ann M. Lees et al.

# NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

Fig. 22 (continued, 5/5)

11000	GGAATTGCTGGTACAAAGACCAAAACAACCAAATGCCACCGCTGCCCTGTGGGTAGCATC	11059
11060	TGTTTCTCTCAGCTTTGCCTTCTTGCTTTTTTCATATCTGTAAAGAAAAAATTACATATC	11119
11120	AGTTGTCCTTTAATGAAAATTGGGATAATATAGAAGAAATTGTGTTAAATAGAAGTGTT	11179
11180	TCATCCTTTCAAAACCATTTCAGTGATGTTTATACCAATCTGTATATAGTATAATTTACA	11239
11240	TTCAAGTTTAATTGTGCAACTTTTAACCCCTGTTGGCTGGTTTTTTGTCTGTTTTGTTT	11299
11300	TGTATTATTTTTAACTAATACTGAGAGATTTGGTCAGAATTTGAGGCCAGTTTCCTAGCT	11359
11360	CATTGCTAGTCAGGGAAATGATATTTATAAAAAATATGAGAGACTGGCAGCTATTAACAT	11419
11420	TGCAAAACTGGACCATATTTCCCTTATTTAATAAGCAAAATATGTTTTTGGGAATAAGTGG	11479
11480	TGGGTGAATACCACTGCTAAGTTATAGCTTTGTTTTTGCTTGCCCTCCTGATTATCTGTAC	11539
11540	TGTGGGTTTAAGTATGCTACTTTCTCTCAGCATCCAATAATCATGGCCCTCAATTTATT	11599
11600	TGTGCTCACCCAGGGTTTCAGAGCAAGAAGCTCTTGCTTTATACAAATGTATCCATAAAATA	11659
11660	TCAGAGCTTGTGGGCATGAACATAAACTTTTGTTCCTACTAATATGGCTCTGTTTGGAA	11719
11720	AAAACCTGCAAATCAGAAAAGATGATTTGCAGAAAGAAAGAAAACTATGGTGTAATTTAA	11779
11780	ACTCTGGGCAGCCTCTGAATGAAATGCTACTTTCTTTAGAAATATAATAGCTGCCTTAGA	11839
11840	CATTATGAGGTATACAACCTAGTATTTAAGATACCATTTAATATGCCCCGTAAATGTCTTC	11899
11900	AGTGTTCTTCAGGGTAGTTGGGATCTCAAAAGATTTGGTTCAGATCCAAACAAATACACA	11959
11960	TTCTGTGTTTTAGCTCAGTGTTTTCTAAAAAAAGAACTGCCACACAGCAAAAAATTGTT	12019
12020	TACTTTGTGGACAAACCAAATCAGTTCTCAAAAAATGACCGGTGCTTATAAAAAGTTAT	12079
12080	AAATATCGAGTAGCTCTAAAACAAACCACCTGACCAAGAGGGAAGTGAGCTTGTGCTTAG	12139
12140	TATTTACATTGGATGCCAGTTTTGTAATCACTGACTTATGTGCAAACCTGGTGCAGAAATT	12199
12200	CTATAAACTCTTTGCTGTTTTTGATACCTGCTTTTTGTTTTCATTTTGTTTTGTTTGTAA	12259
12260	AAATGATAAAACTTCAGAAAAATAAAATGTGAGTGTTGAATAATTTATTTTTCTCTGACAC	12319
12320	TTTAAACAATTATGAATGTATGGTTAATTAAGAGGAAGGTTTTCTGCTTCTACCACCAAG	12379
12380	TACTGTACTCTTAACAAGAACAGTTTTGGTAGGGTTTTTATAAGACTATATAGATTAAGA	12439
12440	TGATAGAGAAGAGAGTCATGAATGATGTGAGAGCACTACTGAAGCCTTTGGAGTGATTCC	12499
12500	ATAGCCTTCTGGATGGCAGCTGAATACCTATATGTAGTATCACTGCCCAAAGACCTAGAC	12559
12560	TAGAAAGTGCAAAGTAGCTTAGCAGCTGCAGTCATTCACTCCAGCCTCCAAATTTCTCT	12619

[illegible]

# NOVEL LOW DENSITY LIPOPROTEIN BINDING PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING ATHEROSCLEROSIS

Fig. 23 (1/6)

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1 - GATCCCTCTCCAGGTGGAAG - 60 / \
61 - CTCCCTTCATACCAAAGTTTAAAGGCCCTGGGGATACGAGTAACTTTGACGACTATGAGG - 120 |
121 - AAGAAGAAATCCGGGTCTCCATCAATGAGAAGTGTGGCAAGGAGTTTTCTGAGTTTTAGG - 180 |
181 - GGCATGCCTGTGCCCCCATGGGTTTTCTTTTTCTTTTTCTTTTTTTTGGTCGGGGGGG - 240 |
241 - TGGGAGGGTTGGATTGAACAGCCAGAGGGCCCCAGAGTTCCTTGCATCTAATTTACCCCC - 300 |
301 - CACCCACCCCTCCAGGGTTAGGGGGAGCAGGAAGCCCAGATAATCAGAGGGACAGAAACA - 360 |
361 - CCAGCTGCTCCCCCTCATCCCTTCACCCTCCTGCCCCCTCTCCCACTTTTCCCTTCCTC - 420 |
421 - TTTCCCCACAGCCCCCAGCCCCCTCAGCCCTCCAGCCCACTTCTGCCTGTTTTAAACGA - 480 |
481 - GTTCTCAACTCCAGTCAGACCAGGTCTTGCTGGTGTATCCAGGGACAGGGTATGGAAAG - 540 |
541 - AGGGGCTCAGCTTAACTCCAGCCCCACCCACACCCCCATCCCAACCAACCACAGGCC - 600 |

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Human cAMP-dependent protein kinase  
catalytic subunit alpha

Accession number X07767 (until \*)

- follow arrow until line that begins 1561 -

begin 1901

```
601 - CACTTGCTAAGGGCAAAATGAACGAAGCGCCAACCTTCCTTTCGGAGTAAATCCTGCCTGGG - 660
661 - AAGGAGAGATTTTTAGTGACATGTTTCAGTGGGTTGCTTGCTAGAAATTTTTTAAAAAAC - 720
721 - AACAAATTTAAATCTTATTTAAGTTCACCAGTGCCTCCCTCCCTCCTTCTCTACTCCC - 780
781 - ACCCCTCCCATGTCCCCCATTCTCAAATCCATTTTAAAGAGAAGCAGACTGACTTTGG - 840
841 - AAAGGGAGGCGCTGGGGTTTGAACCTCCCCGCTGCTAATCTCCCTGGGCCCCCTCCCCGG - 900
901 - GGAATCCTCTCTGCCAATCCTGCGAGGGTCTAGGCCCTTTAGGAAGCCTCCGCTCTCTT - 960
961 - TTTCCCCAACAGACCTGTCTTCACCCTTGGGCTTTGAAAGCCAGACAAAGCAGCTGCCCC - 1020
1021 - TCTCCCTGCCAAAGAGGAGTCAATCCCCAAAAGACAGAGGGGGAGCCCCAAGCCCAAGT - 1080
1081 - CTTTCTCCAGCAGCGTTTCCCCCAACTCCTTAATTTTATTCTCCGCTAGATTTTAAC - 1140
1141 - GTCCAGCCTTCCCTCAGCTGAGTGGGGAGGGCATCCCTGCAAAAGGGAACAGAAAGAGGCC - 1200
1201 - AAGTCCCCCAAGCCACGGCCCGGGGTTCAAGGCTAGAGCTGCTGGGGAGGGGCTGCCTG - 1260
1261 - TTTTACTCACCCACCAGCTTCCGCTCCCCCATCCTGGGCGCCCCCTCCTCCAGCTTAGCT - 1320
1321 - GTCAGCTGTCCATCACTCTCCCCACTTTCTCATTTGTGCTTTTTTCTCTCGTAATAGA - 1380
1381 - AAAGTGGGGAGCCGCTGGGGAGCCACCCCATTCATCCCGTATTTCCCCCTCTCATAACT - 1440
1441 - TCTCCCCATCCCAGGAGGAGTTCTCAGGCCTGGGGTGGGGCCCCGGGTGGGTGCGGGGGC - 1500
1501 - GATTCAACCTGTGTGCTGCGAAGGACGAGACTTCCTCTGAACAGTGTGCTGTTGTAAAC - 1560
1561 - ATATTGAAAACTATTACCAATAAAGTTTTGTT*TAAAAAAGAGTGTCTGGTGGTCTC - 1620
1621 - GACTTCGATCACCCACCCACACACCCCCAGGGGTTGAAAAAGGAATTTTCGGACCCACG - 1680
1681 - GTGCAGGCCGATCAGGTCTCGCTTGAAGTCCTTGTAACCAGGGTTTAGCTGAAATTCG - 1740
1741 - GCACTCCTTCGGCCCCGAGGAGAAACGAGCGTCAAACCTGCCCTTTGACCCAGATTTCGG - 1800
1801 - GGTCCCCAAATCTGCGGCGCGCCCCCTCGGCGTCCAGCCCGGACCGAGAGGGCGCTCTA - 1860
1861 - GGGAGGCGCTGGGGCTGGCGCGCCAGGAGGCCGAGCGGCGGGGGCGGCCCTGGCAGG - 1920
1921 - GGGAGTAGAAGGGGGAGAGGGTGC GCGCCCCCTTCCCGCATCCTCAGCGCCGGGCCAGG - 1980
1981 - CGCGCTGAGGGACGCGGGGGCGGCGGCAGCAGGAGGGTCCCCGCAGCACCTGCGAGCG - 2040
2041 - CGGCAGCCCCGCCCCGCGGGCGGCGAGTTCCCGGTAAGTGC GGTCCCGAGAGCGGAGCGC - 2100
2101 - GCTGGAGAGCGTGGAGAGGGGGGCTGGGCGCCGGGGACGTCTGGGTCCCGCGCCCAATG - 2160
2161 - GCTGGAGGGCGGCCGAGCGCCGCCGCCGCCCTGCCCGCCCCCTCCCCCTCCCCCGG - 2220
2221 - CACTCCCCCTCCCCCTCCCCCGCCCGCGCTTTCCCCCGCCCCCGCCCCGCGCCAACTCC - 2280
2281 - GCGGCGCTCCTTAAAAAGCGCGCGGGAGTTGTAAGGGGGGGCCGGAGCGAGCCGGAGTG - 2340
2341 - AGCGAGAGCGCAGGGTAAAGGGGGCGGGCGGGGGGCCCGGCTCCACCTTAAAGCGGGC - 2400
2401 - GCGTGGGGGTGGGAGGGAGGAAGGCGGGCGGCGGGGAGGAGGGAGGGAGGAAGGAAGGG - 2460
2461 - GGGCCGAGTGTCCCGGGCGCAGGGCGCGCGTGC GCGCGCGCGCGCGGGGAGGGGCC - 2520
2521 - GGCCGCGCGCGCTCCCCCTCTCCCCCTCGCATCCCCGGCCCCGCGCGCGCCAGCAGAA - 2580
2581 - GCGGGTCTGTGTGTCGTCGTCGAGTGAGTGAGTGTGTCATATTTTTTCTCTCTTTT - 2640
2641 - TCTTTCTCTCTACTGTTTTTCTCTCTCTCTCTCTCTCTCTCTCTTTT - 2700
2701 - TTTTTTTTTTGCAAGAAAACAGCAGCGCGCGCGCGCTCCGCCGAGGCGTGC GCGCCCC - 2760
2761 - GGGGGGGGAGGCGGAGGAGGCGGGCAGCGCGGAGGGAGGGGAGCGGGGAGGGGGCGC - 2820
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[illegible]

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— fig. 23 (continued, 2/6) —

2821 - CGCGCTGGGAGGGAGGCAGCGCGCACGGTGCAGCCGGGCGGGGCGGAGGCATGGCGGGG - 2880  
- M A G

2881 - CCCCCGGCCCTACCCCCGCGGAGACGGCGGGCGGCCACCACGGCGGCCGCCCTCG - 2940  
- P P A L P P P E T A A A A T T A A A A S

2941 - TCGTCCGCCGCTTCCCCGCACTACCAAGAGTGGATCCTGGACACCATCGACTCGCTGCGC - 3000  
- S S A A S P H Y Q E W I L D T I D S L R

3001 - TCGCGCAAGGCGCGGCCGACCTGGAGCGCATCTGCCGGATGGTGCGGCGGGCGGCACGGC - 3060  
- S R K A R P D L E R I C R M V R R R H G

3061 - CCGGAGCCGGAGCGCACGCGCGCCGAGCTCGAGAACTGATCCAGCAGCGCGCCGTGCTC - 3120  
- P E P E R T R A E L E K L I Q Q R A V L

3121 - CGGGTCAGCTACAAGGGGAGCATCTCGTACCGCAACGCGGCGCGGTCCAGCCGCCCCGG - 3180  
- R V S Y K G S I S Y R N A A R V Q P P R

3181 - CGCGGAGCCACCCCGCGGCCCGCGCGCGCCCCCGGGGCCCCCGCCGCCGCCGCC - 3240  
- R G A T P P A P P R A P R G A P A A A A

3241 - GCCGCCGCGCCGCCGCCACGCCCGCCCCGCCACC GCCCGCGCCCGTCGCCGCCGCC - 3300  
- A A A P P P T P A P P P P P A P V A A A

3301 - GCCCCGGCCCCGGGCGCCCCGCGCGGCCGCCGCCGCCACAGCGCCCCCTCGCCTGGC - 3360  
- A P A R A P R A A A A A A T A P P S P G

3361 - CCCGCGCAGCCGGGCCCCCGCGCGCAGCGGGCCGCGCCCCCTGGCCGCGCCGCCGCCGCG - 3420  
- P A Q P G P R A Q R A A P L A A P P P A

3421 - CCAGCCGCTCCCCCGCGGTGGCGCCCCCGGCCGCCGCCGCCCGCGCGCCCCCGCCGCC - 3480  
- P A A P P A V A P P A G P R R A P P P A

3481 - GTCGCCGCCGGGAGCCGCCGCTGCCGCCGCCGCCACAGCCGCCGGCGCCGCCACAGCAG - 3540  
- V A A R E P P L P P P P Q P P A P P Q Q

3541 - CAGCAGCCGCCGCCGCCCAGCCACAGCCGCCGCCGGAGGGGGGCGCGGTGCGGGCCGGC - 3600  
- Q Q P P P P Q P Q P P P E G G A V R A G

3601 - GGCGCGGCGCGGCCCGTGAGCCTGCGGGAAGTCGTGCGCTACCTCGGGGGCAGCGGCGGC - 3660  
- G A A R P V S L R E V V R Y L G G S G G

3661 - GCCGGCGGTGCGCTAACCCGCGGCCGCGTGCCAGGGGCTGCTGGAGGAGGAGGCGGCGGCT - 3720  
- A G G R L T R G R V Q G L L E E E A A A

3721 - CGAGGCCGTCTGGAGCGACCCGTCTCGGAGCGCTTGCGCTGCCCCGCGGGGACAGGCC - 3780  
- R G R L E R T R L G A L A L P R G D R P

3781 - GGACGGGCGCGGCCCGGCCAGCGCCCGCCGCTCTCGCAGCAAGGTGAGCGCGCCGGG - 3840  
- G R A P P A A S A R P S R S K

3841 - AGCGGGGGCGCCGCGCGGTGGGCAGGTGCGGGCGAAGTTGGTGGCGGGGGCGGAGTCCC - 3900  
3901 - GGGAGGAAGTGGGTGGCGGGTGGCTGGGGCTTTGCGCGCGTTTCTGCGGGCTCGGTGCG - 3960

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Fig. 23 (continued; 3/6)

3961 - TGGTGACCTTGGCAAGTGATTGAATCTCCCGGAGCCTCAGTTTCCTCCGCTGTAAACGCG - 4020  
 4021 - GTTTAATAACAGTAGCGACCCCTTGGGGTTGTTGAGCGAGTTTAGTAAGATTTGGTTGTC - 4080  
 4081 - GAGGGCTTTAGTTAACACAGAGCCTGGCACGGAGTGAATGCGTAAAAGTTAGTCCGTATT - 4140  
 4141 - GTTCTTAAAGGTGGAATCGGTTCTCTCTCCCCACCGCCCGGACGCCACAGTCAGGGTCTG - 4200

4201 - GGATTAGAACAGCTACTAATTTTGCATGCTTCTCTCTCTCGGCTCCAGAGAGGTGGAGAAG - 4260  
 - R G G E E

4261 - AGCGAGTACTTGAGAAAGAAGAGGAAGAAGATGATGATGAAGATGAAGATGAAGAAGATG - 4320  
 - R V L E K E E E E D D D E D E D E E D D

4321 - ATGTGTCAGAGGGCTCTGAAGTGCCCGAGAGTGACCGTCTGTCAGGTGCCCAGCACCACC - 4380  
 - V S E G S E V P E S D R P A G A Q H H Q

4381 - AGCTTAACGGCGAGCGGGGACCTCAGAGTGCCAAGGAGAGGGTCAAGGAGTGGACCCCCT - 4440  
 - L N G E R G P Q S A K E R V K E W T P C

4441 - GCGGACCGCACCAGGGCCAGGATGAAGGGCGGGGCCAGCCCCGGGCAGCGGCACCCGCC - 4500  
 - G P H Q G Q D E G R G P A P G S G T R Q

1 - AGGTGTTCTCCATGGCAGCCATGAACAAGGAAGGGGAACAGGTAAGGATCCCTCTGGGT - 60  
 - V F S M A A M N K E G G T

61 - GGGGAAGAGTGCTAGGTGGAGAGGAACTCAGCCCCAAGACAAAGCCAAAGACAGGTGTTT - 120

121 - TTTTCCTTCCCAGCTTCTGTTGCCACCGGGCCAGACTCCCCGTCCCCCGTGCCTTTGCCC - 180  
 - A S V A T G P D S P S P V P L P

181 - CCAGGCAAACCAGCCCTACCTGGGGCCGACGGGACCCCCTTTGGCTGTCCGTAAGTTGGG - 240  
 - P G K P A L P G A D G T P F G C P

241 - GTATTGGAGACATGGGGGTGCTGCTCAGGTGTGTGGTACAGCCAGAGAGACATCCGTGTT - 300

301 - CACTGGTGTCTGTTTGTGTTTGTGATGCAGTCCCGGGCGCAAAGAGAAGCCATCTGATCCCGT - 360  
 - P G R K E K P S D P V

361 - CGAGTGGACCGTGATGGATGTCGTCGAATATTTTACTGAGGCTGGATTCCCGGAGCAGGC - 420  
 - E W T V M D V V E Y F T E A G F P E Q A

421 - GACAGCTTTCCAAGAGCAGGTGAGTTTCCAGCCCAGGACTACACACTGACAGACACAGAG - 480  
 - T A F Q E Q

481 - GGCCTCCCTGGGATGTGCCCTGATCCCGGCTTTCTCTGTTCTGTCCACCCAGGAAATT - 540  
 - E I

541 - GATGGCAAATCTTTGCTGCTCATGCAGCGCACAGATGTGCTCACCGGCCTGTCCATCCGC - 600  
 - D G K S L L L M Q R T D V L T G L S I R

601 - CTCGGGCCAGCCCTGAAAATCTACGAGCACCACATCAAGGTGCTTCAGCAAGGCCACTTT - 660  
 - L G P A L K I Y E H H I K V L Q Q G H F

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fig. 23 (continued; 4/6)

661 - GAGGATGATGACCCCGATGGCTTCTTAGGCTGAGCGCCAGCCTCACCCCTGCCCCAGCC - 720  
- E D D D P D G F L G \*

721 - CATTCCGGCCCCCATCTCACCCAAGATCCCCAGAGTCCAGGAGCTGGACGGGGACACCC - 780  
781 - TCAGCCCTCATAACAGATTCCAAGGAGAGGGCACCCTCTGTCTTATCTTTGCCCTTG - 840  
841 - TGTCTGTCTCACACACATCTGCTCCTCAGCACGTCGGTGTGGGAGGGGATTGCTCCTTA - 900  
901 - AACCCAGGTGGCTGACCCTCCCCACCCAGTCCAGGACATTTTAGGAAAAAAAAAATGAA - 960  
961 - ATGTGGGGGGCTTCTCATCTCCCCAAGATCCTCTCCGTTCCAGCCAGATGTTTCTGTAT - 1020  
1021 - AAATGTTTGGATCTGCCTGTTTATTTTGGTGGGTGGTCTTTCCCTCCCTCCCTACCACCC - 1080  
1081 - ATGCCCCCTTCTCAGTCTGCCCCCTGGCCTCCAGCCCTAGGGGACTAGCTGGGTTGGGG - 1140  
1141 - TTCCTCGGGCCTTTTCTCTCCTCCCTTTTCTTTCTGTGATTGTGCTCCAGCTGGCTG - 1200  
1201 - TATTGCTTTTAAATATTGCACCGAAGGTTTTTAAATAAAATTTTAAAAAAGAAAAAGG - 1260  
1261 - GAAAAAAGCCACGGAGTCCATTTTATGAATGGGGTGGGGAGAGGGCACTAAAGAGCCT - 1320  
1321 - CCTAAGAGAGCCTCAGGTTAGGACAGAATTGTTTGGGGAGGGAGAAAAACAGAAACAATG - 1380  
1381 - AATTATAGCTGCCTCACAGCCATGTATAACAATAATTGCTCCAGGAAGGTGGGAATATTT - 1440  
1441 - GCTTTTTTTTCTTCTGTAATCTCACCGTGTCCGTGTCCAGAACAGAGCTAGGCACACAGC - 1500  
1501 - AGGTGCTCAATTTTTGTTTTTCGTTTAGACAGGTTTCATTCTTTACCCAGGCTGGAGTG - 1560  
1561 - CAGTGGTGCTATCATAGCTCATTTGTAGCCTCAAACCTCCTGGGCTGAAGTGATCCTCCCAC - 1620  
1621 - CTCAGCCTCCTGAGTAGCTGGGACTACAGGTGCACTCTGCCATGCCGGGCTAACTTTTAA - 1680  
1681 - AAATTTTTGTCCGGGCACAGTGGCTCATGCCTGTAATCCCAGCACTTTGGGAGGCCGAGG - 1740  
1741 - TGGGTGGATCATGAGGTGAGGAGTCAAGATCAGCCTGGCCAAGATGATGAAACCCTGTC - 1800  
1801 - TCTACTAAAAATATAAAAAAAATTAGCTGGGCGTGGTGGTGGTGCCTGTAATCCTAGC - 1860  
1861 - TATTCAGGAGGCTGAGGCAGAGGATTGCTTACACCTGGGAGGCGGAGGGTGCAGTGAGCC - 1920  
1921 - AAGATCGTGCCACTGCACTCCAGCCTGGGTGACAAAGTGAGACTCTGTCTCAAAAAAAA - 1980  
1981 - TCTTTGTGTGTGTGTGGAGATGAGGGTATGCACTTTGTTGGCCAGGTTGGCCTCGAACTC - 2040  
2041 - CCAGCCAAGCAATTCTGCCTGGGATTACAAGCGTGAGCCACCATGCCTGGCCTCAAATAT - 2100  
2101 - TGTTGAATGGCTAGCAGTTAAGTCCTTGGGTTTATAAGCATTTCTCAACTGTCCTCCCA - 2160  
2161 - AGTCCCCATAAGACAAAAAACTCATAAAATCCACCTTACAGAAGAGGCAGCTGGCCCCG - 2220  
2221 - CACAGAGATGCTGTCTGCCCCGGGTACACAGGGTGGCATCTGACACCCTGTCTGAGTTC - 2280  
2281 - TTCACTCAGAGTCTTTAAATATAATTAGCGTATTTGACATAATGTACATTA AAAA CTATA - 2340  
2341 - AACCTGTCAGCCTTTGTCTACTGCAAAGAATCCACTACAAATATTGGGGCAGGGATCTGT - 2400  
2401 - TCCTGGACCATAGTAGTGTCTCCAGACCTCATGGTCCTCTTCATTAAACAACAGAAAAT - 2460  
2461 - TCCTTCTGGGCCATCAGATGAGACCATGAGATAGAAGATTTCCAAGTGAAGATTTTGT - 2520  
2521 - CAAGACAGAGTCTTGCTCTGTCACTCAGGCTAGAGTGTAAGTGGTGAATCATAACTGTGG - 2580  
2581 - TGACAGCCTCGAACTTTTGGGTACAAGTGATTCTCATGCCTCAGACAACACCCAATAAT - 2640  
2641 - ATTTTGGTTTTTGTATAGACAGGGTCTTGCTATGTGGCTTAGGCTGGTCTTGAACCTCTG - 2700  
2701 - GCCTCAAGCAGTCTCCCGCTTCAGCCTCCTAAAGTGTGAGGATTACAGACATGAGCCAC - 2760  
2761 - CAAGTCCAGCCTGAAGATTTTAAAAATATTGTTAGTAGTAGTCGCCAGAGTTACTACA - 2820  
2821 - TCCAAAGTCCCTACTAAGTTCTAAGTAGTCCCTACTAAGTTCTAAGGCAGTTTCTCAACT - 2880  
2881 - CATTAGAGTTGTTTTTGTTTTTTAAAGAAAAAAGAGGCTGGGCACTTTAGGAGACCGAC - 2940  
2941 - ACGGGAGGATCGCTTGAGTCCAGGAGTTTGAGACCAACCTGGGCAACATGGGCCCCCATC - 3000  
3001 - TCTAAAAATTTTAAATTA AAAA ATGTTTTAACAACAAAAAGCGTTCTGGGAGTGAGGGG - 3060  
3061 - CTGGGGCCTGGGCGGCCTCATTCATATACCTGTGCCGGGTTGAGGGGTTGGAGACACGT - 3120  
3121 - TTAGAGACCCCTCCACTCTAGGAATCCACCTCGAGAGATAAAGGTCCCGGCCCTAGCCAC - 3180  
3181 - ACCCCCAGGACACGGCCAGAGGCCACCTCCCTAGGCGGGTCCCTCCCCACCGCCAGGTT - 3240  
3241 - CTGGAGCGGTGCGGCGCGTGTGACAGGGGTAGGGGGCCGAGGCGCGCGGACTGGAGAGG - 3300  
3301 - CGCGCCCCCTCCCGGTGTTGAAATTCAAAGAGGCGAACGGCCCCCGGCGCGGCGGCGG - 3360  
3361 - GCTCCGGTGGAGAGGTCAAGGCAGGGGCCAGTCGGAGGCTCCCGGGGCGGGGTGCAACCC - 3420  
3421 - GCGGCCAACCTGAGCAGCAGCGGAAGCTTAAAGAGCTCAGGTTCCCGCCCCCGGCCCTA - 3480  
3481 - CCATGGCTACAGAGCAGTGGTTCGAGGGGTGCTCCCCCTGGACCCTGGAGAAACACCGC - 3540  
3541 - CTCCAGACGCCTTGGAACCTGGGACGCGCGCCCTGCGGAGACCCCTCCAGGTCGACGCCCC - 3600  
3601 - CTGGCAGGCCTGGGAACCCATCTGAGCCGGATCCTGAAGATGCCGAGGGGCGGCTGGCTG - 3660  
3661 - AGGCCCCGGGCCTCCACGTCTTCCCCCAAACCTCTGGTCCCCCGGCCTGGGCCAGCACCTC - 3720



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--- Fig. 23 (continued, 5/6) ---

3721 - CCCGCCTATCCCTGGACACTTTGTTCAGCCCCATCACCCAACAGCTGCGCTACCTACTGA - 3780  
3781 - AGAAGGCAGATGATTTCCAGAGCTACTTGCTCTACAGGTGATGCTGGACAGGGTCCCAGG - 3840  
3841 - TCCCCATGGGTAAGGAGACTTGGAGGGGAGGCGACAGGATGGGTGACACACACCAGGGTC - 3900  
3901 - GCAAAATTACAAGCGCTAGGAGCCAGAGGGAGACAGTGAAGAAGCTAGCATATTAGAAT - 3960  
3961 - CCAGTTTAAGAGAATGAGGAAGACTGTAGAATTGCGGGTAGGGGATGGCTGCTATTACTG - 4020  
4021 - TCGTGGCAGGGTGGGCCTGGGGTTGTCAAGTCTCTAGGACTTTTTCTCCAGTTTTTAAG - 4080  
4081 - TGCTGTCTTACATTTTGGCCCTGTGCTGGCTAAACAAGACCCACCTGAGCCAAACTTGG - 4140  
4141 - CCTGCAGGACATCAGTTTGGAGCTCCAAAGGATAATGTGATTCCCAGACCAGGTTTCCCT - 4200  
4201 - GTGACTCTCAATTTCACTGTCCATTGGAATTTCTAGGAGGCTGGGTTGGGTTTGGTTTGC - 4260  
4261 - GTGTTTGTGTTTTGAGATGGAGTCTCACTCTGTGCGCCAGGCTGGAGTGCAGTGGTGCAAT - 4320  
4321 - CTCAGCTCACTGCAACCTCCGCCTCCCGGATTGAAGCAATTCTCTGCCTCAGCCTCCCGA - 4380  
4381 - GTAGCTGGGATTACAGGCGCCCAACATGTGTTGCCCGGCTAATTTTTTCTTTTCTT - 4440  
4441 - AGTAGAGACAGAGTTTCAACCATCTTGCCAGACTGGTCTTGAGCTCCTGACCTCATGATC - 4500  
4501 - CACCCGCCTTGGCCTCCCAAAGTGCTGGAATTACAGACGTGAGCCACCGCGCCTACCCGA - 4560  
4561 - GGCTGGGTTTTTTTGTGTTTGTGTTGTTATGTGTTTTTTTGAAATGGAGTCTTGCTCT - 4620  
4621 - GTCACCTAGGCTGGAGTGCAGTGGGGCGAACTCAGCTCACTGCAACCTCCGCCTCCCAGG - 4680  
4681 - TTCGAGGGATTCTCATGAGGCTGTTTTTTTTTTTTTAATGAGACAGGGTCTCGCTCTGTC - 4740  
4741 - ACCCAAGCTGGAGTGCAAGTGGGCGAGTCATGCTCACTGCACCCTCGAACTCCTGGTCT - 4800  
4801 - CAAGCAATCTTCCACCTCCCTCCTGGGTAAGTGGGACTACAGGTGCCACCATGCCAGC - 4860  
4861 - TAATTATTTTTGTGTAGAGATGGGTCTTGCTATGTTGCCTAGGCTTGCTGGAACCTCT - 4920  
4921 - GGCTCAAGCAATCCTCCAGCCTCAGCCTCCCAAACTCTAGGATTGCAGGCGTGAGCCA - 4980  
4981 - CTGTGCCCAGACCTTCAGGAAGCTCTGGGTCTAAGTGTTGTGACACTCAGGTGTCAGC - 5040  
5041 - ACTTTAAACAAGTGTTCAAATGGGTTTGATGCAGGTAAACCAGAAAGATGTTCAAGAAAG - 5100  
5101 - ACCTGAACTGGGGGCTTTTCTAATGGGTCAAAGCCAGGGATACAGGTTGGGATTGAGTA - 5160  
5161 - GAATGGGGAAAAGTGGGGGTGGGGAGGGGTTGTGAGGGATTCCAGGCAAAGGCCCTT - 5220  
5221 - CTTCTTCAGCAGAGACCAAGTACAGAAGGAGCAGCTGGCCAAGGCCATGCCACCTTCT - 5280  
5281 - TACAGATGTGTGAGCCCTACTTCTGTACCTGGAGGCAGCCGCGAGAAGCATACCCCCCA - 5340  
5341 - TCTATGGACCCCTGCAGGAGCTGGTCCGAAAGGGGGTGTGTGGAGGTTTCTTAGACCCCA - 5400  
5401 - CGCCCTTTCTTCTCGCAGCTCTGAGCCTGTGGGGATGGTGGAGGGGGAGGCCACTCCT - 5460  
5461 - CGCAGGCCAGCTGATCTCACTGTACCCCCCTCTTGATGCAGCTGTTAGAGATCTCCCAA - 5520  
5521 - CAGCTGACCCCTGCGCCTGGAACAGCTGGTCCTCATGTACGCTTCTTTGGGTTTCGTGGAC - 5580  
5581 - CTGGAGGAGATGAACCCCTTAGGTAAAATGGTAGGAGACTCAGATGGGGGGATGAAGGA - 5640  
5641 - GTCCAAGGCCAGCCTCACCCCTCCATTCTCTCATGTCTCGCCAGCATCTCCTGTTTCTT - 5700  
5701 - TTGCGGGAGGTTCTCCATCAGCCTGTCCCATGAGGTCTCCATCTTCAAGATACTGTGCCCC - 5760  
5761 - AACCCTTACACTGCCAGCCGCTTCCCCGCTACCTCTATAAGAAGATGCGCTGGCACCT - 5820  
5821 - GGAAGCCACCCAGAGGCCCTGTGTCGGGGACAAGATTCCCTTGTGGATTAGTAAGTCTT - 5880  
5881 - CTTACCCAAATCAAAGTCCCTCCCTTTCTATGATGAATGCCAATATGACCTCCAAACCG - 5940  
5941 - TCACCAGCAAAGTGAAAAGTGAAGCCAGGGCCCCGAGGCAGTGGCTCACGCCTGTAATCCCA - 6000  
6001 - ACACTTTGGGAGGCCGAGGCAGGAGGATCACTTGAGCTCAAGAGTTTGAGATCAGCCTGG - 6060  
6061 - GCAAGATGGCAAGACCCTGTCTCAACAACAAAGAAATTCGCCAGGCGTGATGGCTGGCAC - 6120  
6121 - CTGTAGTCCCAGCTACTTGGGAGGCTTAGGCAGGAGGAGCACTTGAGCCCAGGAATCAAG - 6180  
6181 - GCTACGGTGAGCTGTGATTGTGCCACTGCACTCCACCCTGAGTGAAGCAATAATCTGTC - 6240  
6241 - TCTTAAAAAAAAAAAAAGTGAACCAGGAACTAAAGGCTTTTGAAAGGCTACCTCTATT - 6300  
6301 - TTCTTAAAACCCACCTCCCAACCAAAATAAAAGTTCTCATCTTAAAAGTAGGCTGGCAGG - 6360  
6361 - GAGAAAAGGCCCTTGGAGTCACATTCTACCTGAGAACTTCAGGGCAACTTCTGATGAGTT - 6420  
6421 - CCCACCTCAACTCCAAAATTAAGCCCTCAACAGAAGTAGCTAGGAAGCTGATCACTTCT - 6480  
6481 - AATTACAGCTCCCTCCCTCCTAGCTACTTTCTGTGCTATCGAGATACTTGGGAAGACAC - 6540  
6541 - AGGCCAGAGTCCAGCCAATTCGTGCCCACAGATCCAGAAGCTGTGGTCCATCGGCCGATG - 6600  
6601 - GGTGCCCTTAGGACCAGCCGAGGATGACCTTTATTTCATGGTAGGAGCTAGGGCAATAGCA - 6660  
6661 - ACGTGGGCTTGGGAGCTGGAGGGGGAGGCAGAACCCACCAAGACAATCCACCTTCCCA - 6720  
6721 - AACACTTTGCTTCCCTTAGTAGTATGATGATGATTTTATTGTGCCCTGAAAAGCACTTCATGC - 6780  
6781 - AGACCCAGTAACAACCCATGGAGATCTATGCTATTGGCCCCATTTAACAAGAAAACAG - 6840  
6841 - GGTGCTCAGAGAAGTTGTTACCTGCCCAAGGACACAGCTAGCAGAGCGAATGGACAGG - 6900  
6901 - TCAGGACCAGTTATTCAGCCTCTAGGAGCCATTACTAAGTCTCTGATCAACAAGGAAACA - 6960  
6961 - AGTTTCCCCCGGGGGTTTTTCCACCCGAGCTGAAACAAAGCCTCTTTCACCTGAGCCT - 7020

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- - - - Fig. 23 (Continued, 6/6) - - - -

7021 - C T C A C T C A A A G G G A G G G A C T C C C G A G G G G C A G G G G C A C T C A A G T C C A G G C C T G T C T A T C - 7080  
7081 - C C T G G C C C C C C A C C C C A G G A T T T T G T G C C C G C A C C G C T T G G G G A C T A C C A G C A G C T G C T - 7140  
7141 - G A C C A T C G G C T T C G A G G A G C C C A C G C C C A C G C T G G C C A C C G A C C T G C T G G T G C A G A T C C T - 7200  
7201 - C A C G G G C C A G G C A G G C C A G G C C C G G C C T C C G A G C G C A G C C G G G C C T G C G G G T G G G C A G C - 7260  
7261 - G C A G G G T C T T G A A C C T G G G G A A G A G G G T A G G A G C T G G A A C T T G A C A G T T C C A A A C T C C A - 7320  
7321 - G A A T A G G G G G C A G G G G A G G G G C T C A C T C G T T C T C G C A G T G C A G C C G G G C C T C G C C T T C C A - 7380  
7381 - A A G G G C C A G G C G A G C T G A C C T G T C T G C A C C G A G T C C G G C T T G G C C G T G G G G C C C T G A A T - 7440  
7441 - G C G G A C A C G T C A G T T T T G T G T T A A A T A A A A G A A A G A A G A G G T C A C A G G C T C A G C G T C C G - 7500  
7501 - C T G C G A A T G C C G C G C C C C T C C C C C G G G G G A T T G C C C C A C C C A C T C G C G T G G C C T T C T G G G - 7560  
7561 - A A A T G T A G T C T T T T G A A A G A A G C C T G G A A T T C G C C A A T A G G C G G A C G A G A G T T T G G C G C A - 7620  
7621 - T G C G C A T A G G C G C A C A T G A A G C A A A A G G G A A G T G G T G C C C G T C A A C A C C G G A A C C C A G A - 7680  
7681 - A A A C T C C A A G T T T A G G G T A C C G G G G A A A T T C A A C G T C C A C T G A G G A G A G A G A C T T A A G G C - 7740  
7741 - T A C G C C C A C T C C C A T A T T T G A C C C G G A A G T T A T T T A T T T T A G C G T A G A A G A C T A C T T T T - 7800  
7801 - C C C G A C G C G C C C C A G G A A A G T G C C C T C G A T C A G T T T C T A A G G G C C C G A G T T A G A C T T T T - 7860  
7861 - T T T T T C T C T T C C A G C T T T T G G G A C T T G G G G G C C G G A C A G G T C G T C G T C T T T C T T G G G G T A - 7920  
7921 - T C C G G G G T G C G G A C A A G G T G G G A G A G C C C T A C G G T A T C C A A G C T T - 7965

[illegible]

Fig. 24 (1/9)

1 - CAACATGCTTGGGACCAGAAGTGTTCCTCAATTTGGGATTTTCTCAAATTTTACCGGTTGA - 60  
61 - GCTTCCCCAATCTGAAATCTGAAATCCAACATGCACGGCTCTGAAGTCTTTCACTGAGC - 120  
121 - CTTTGGGGGAAATATTTAACATCCTAACAGCCCTAAACCAACGCTCAATTAGCACAACAG - 180  
181 - TTTACAATCTTCTCTACCCACAGCCTGATGCGAGGCTCTGGGACTAGACTATTTAGCCAA - 240  
241 - CAGTTCTTGCAAAATTAAGTACTGACTTATAAGTAAATAGTAATTTCAACACCTCACTGCTAA - 300  
301 - TGCTGTAACAACCTCTGCAGACCTAGGGAGCAAGTACGGTTTGCAGAGCACTGGGAAGGCT - 360  
361 - CTGAAGTGACCTTTGAAGTGGGCCTCAAAAAATTTGGGTTTGGCAAAAGTCAAATCTCT - 420  
421 - TAGGCTTCAAATCCAGGCACAAGGATTGTTGGGTTTGAATTCATTATCCAGAAGCAATG - 480  
481 - GGGATACAGAATTGTGATCTCATGTGTAGGGAAGTGTGGGGTTTTTCTACTTTAACCC - 540  
541 - CAGTGAGACTTTGTAGAGTGTGGGGTAGAGAAAAGGCTCATGAATATGCCTGAAGCCTAA - 600  
601 - CTCAGCACCTTTCTGAGGAAGTACTGCCAAAATGGTAATGGAGAGGGGAAAATATGACC - 660  
661 - TACTTTTACAAGTTACCTTGACTGCCTCAGGGAAACCTGCTGTGGTAGTGTTCCTCTGG - 720  
721 - GTGAAAGACCAGGTAATTACCTGGGTGCTGGTCTCAGACTTACCAGTTTTGAATCCCTGT - 780  
781 - TTTAACCCTCACTATCGATATGACCTTGATAAGTTACCTAACCTTTCTCTTACTGTCC - 840  
841 - TTTTCCGTAATAATGGGGATAACAGATAGTAGTTATTTCTATGAGTGGTTATGAGAACCAA - 900  
901 - GCTATTAGATAGCGGGAAGCACACAGTAAGCGTTCAAGGAAGTCTATTGTTATTAATA - 960  
961 - GCCTCCTTTGGAAGAAGGACATTGAGGCCAGAGAGAGAACAGAACGTCAGCCACACAG - 1020  
1021 - CAAATCCGTGATGAAGTTGGGACTGGAGTATGGGTCTCCTGAGTCTCAGCCAGGACTCT - 1080  
1081 - ATCCCTCTTCCCGAGTCTCGGAGTTCCCGGATGGAGTACATTTGTTTACGGCCAGGGA - 1140  
1141 - GGAAGGTTTGATGGAGGCTGCAGGAAACAACAGCCAGGCGCAAGGCTTTGGGAGTTGAA - 1200  
1201 - GCATAGCTTCTGCGAGATAGAAACAAGGTTGACATGGGCACTCGTGCAGAATGACGGGCT - 1260  
1261 - CCTTTTGGACTCCCAGGACTACAGTCCCTTATGCACCTTGGGATCTGCGGCTAGCCCCTG - 1320  
1321 - CGTAAAGAGGGACGCGTAGTCTTTTCCCTGCCCGCCCTGCCGGGCGCCCGCCTCCGAG - 1380  
1381 - GCCGCCCTCGCTTCGTCTTCCAGCAAGCTCCGCGCCGCGCCGCTATTGATTGGCTG - 1440  
1441 - AGGCGGGAGCAGGCGGCTGGCCGCGCAGCAGTTACTCGGGTTTCCGGTGCAGGCCAGAG - 1500  
1501 - GTGGGGAAGCCATCGGACGTCGCGGCTGAGGTACGTGCAGCGGCGCGGCTGGGCGAGAC - 1560  
1561 - TATTTGAGAGTGTGCGGGCCGGATGTTCTCGGCCTGTGGGGAAATCACGCCAACTCCCC - 1620  
1621 - GCGTGGGCGGGGGCTGTCTGGGATATGCGCATGCGCGGGCGTGCCTCGCGGCTTGAGG - 1680  
1681 - GCGCGCGGGGCGTGGGTGGCTGCGCGCGGGGGGCGCACGTGGGGCCTGAGGGGCGGGG - 1740  
1741 - GCGGTGCCGGGAGTCCCGCCACGTACGTCTCCGGCCCTGAGCCAATCCCGCGCCCGGCT - 1800  
1801 - GCCGCGAGGGGGCGGTTGTGCCGGGAAGTGGCTCCAGGGAGAAGAGGCCTCTTCCCTCA - 1860  
1861 - CCCGCTGTGGGAGCTGCGCCCCGAAAGCCTGCCCGGCGCACGTGCGGCTCTCCTGACCCGC - 1920  
1921 - CAAGACCAGAGAGCCGTTGGCGCCCTCCGCCCCGGGCTGCCGGTCCGTTTATTTTAAGAA - 1980  
1981 - GCTTTGTGCGCTGCTGTGGGGATTTCTGATCCAGGCTGCGAAGAATTTCAAGTCTGGA - 2040

2041 - AAATAGCAACTGTGTTTGTTCCTAAAGGATCTTCTCCTGACCCAGCATCGCTCATCACA - 2100  
- M

2101 - TGAAGAACCAAGACAAAAAGAACGGGGCTGCCAAACAATCCAATCCAAAAAGCAGCCAG - 2160  
- K N Q D K K N G A A K Q S N P K S S P G

2161 - GACAACCGGAAGCAGGACCCGAGGGAGCCAGGAGCGGCCAGCCAGGCGGCTCCTGCAG - 2220  
- Q P E A G P E G A Q E R P S Q A A P A V

2221 - TAGAAGCAGAAGGTCCCGGCAGCAGCCAGGCTCCTCGGAAGCCGGAGGGTGTGTGCCAGC - 2280  
- E A E G P G S S Q A P R K P E G

2281 - TCTGCGTTGCCAGCGGGCAGGGGAGGAGCTGTGGGGTGGCCCTCGCTTCTGGACTTACA - 2340  
2341 - GGCCGAGGCCAGGTTGTCCGGGAGGAGAGATGTAGAATGAGAGGACAGTGCTGGGGGCC - 2400  
2401 - GCGGTCCCCCTGCGCTCTGGCGAGTTGGCGGAGCTGCCCCCTCTAAGCACAGGAACAGA - 2460  
2461 - GTTCTGGAGAGAAGCTCCGACGGGATTAAGTCAGGTGGCAGCCAAACGAGGCACCCAGTC - 2520

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- - - Fig. 24 (continued, 2/9) - - -

2521 - AGGAAATCCAGGTCCCCTTAGAAACACCTCAGCCACCAGCAGCTAACTGCCCTTCCTGTT - 2580  
2581 - TGAGGCATTTCTAGAATGATCTGAATGGCAAGAAATGGGTTTGTGGGGGGAAGGAGAT - 2640  
2641 - GGACTAGAAGTTGCTCCGTGCCATCCCTGTGTGCTGATGCTTTACATACTTTTATGATCT - 2700  
2701 - AACAAATATGTTCCGGTGGTAGTGAGAAATAGTTGTGTCATTTTACAAGTAAACAGACTT - 2760  
2761 - AAAGAAGTTAGGCAACGATTACTATAATTTCTTGATTTAAAAGATGTTTCGAATCTAAAT - 2820  
2821 - TCTGACAGGAAGTAGATTTGCTGAATGATACTCCATTCTTGCTTCTCAGTTTCCATAAAA - 2880  
2881 - AAAAAAGTTAGGCAACATTTAACTCAAACGATGAGTTTGGCTGGGCCTGAAAAATCCCA - 2940

2941 - ACCAGTGGTATAATCGTCTTCTTTCTCACTCTACCCCTCATCCTCTCCTGCTGTAGGGGC - 3000  
- A

3001 - TCAAGCCAGAACGGCTCAGTCTGGGGCCCTTCGTGATGTCTCTGAGGAGCTGAGCCGCCA - 3060  
- Q A R T A Q S G A L R D V S E E L S R Q

3061 - ACTGGAAGACATACTGAGCACATACTGTGTGGACAATAACCAGGGGGGCCCCGGCGAGGA - 3120  
- L E D I L S T Y C V D N N Q G G P G E D

3121 - TGGGGCACAGGGTGAGCCGGCTGAACCCGAAGATGCAGAGAAGTCCCGGACCTATGTGGC - 3180  
- G A Q G E P A E P E D A E K S R T Y V A

3181 - AAGGAATGGGGAGCCTGAACCAACTCCAGTAGTCAATGGAGAGAAGGAACCCTCCAAGGG - 3240  
- R N G E P E P T P V V N G E K E P S K G

3241 - GGATCCAAACACAGAAGAGATCCGGCAGAGTGACGAGGTCCGAGACCGAGACCATCGAAG - 3300  
- D P N T E E I R Q S D E V G D R D H R R

3301 - GCCACAGGAGAAGAAAAAGCCAAGGGTTTGGGTGAGCAGAGGGCGGCTCTTTGTGAAGC - 3360  
- P Q E K K K A K G L G

3361 - TGGTGAGGAGAGGGAGTTTGGACTTGACGTTCTCTGGGCCAGTCTGTTCTGCCAGGATTC - 3420  
3421 - AAAGGAAAACGGTACTTCTCAGAGCAGCAAGTCACTCTAGTCTAATCAAAGCCAGGGATG - 3480  
3481 - TGGGGGCCACGGCATAGAGAGATGCAGGAGTTACCAGCACAAAGCCTTCTGGGTTTGGGA - 3540  
3541 - GCAACTGGAGCTTGGCATGGGACCTGTCTCTCTTTGAGAAAATGGAGACGGGAGGCTAG - 3600  
3601 - GGTAGGCTCCTGTGCCAGCCAGTACTACCTGCTGTGTGACCTTGGGTGTGTCCCTTCTCC - 3660  
3661 - TCTCTGGGTCTTAGTTTATATTTCTCTTTACAGTAAGAAAAATTAGACTAGGCCAGAGTTG - 3720  
3721 - AAAACCCAAATATCTGCATAAGCTGGGCTTGGCCATGGGGCCACCTGAAGATGGAGGCTT - 3780  
3781 - TACTGCTTCCCTGATTAGTTGCTCTCACTAGCCAAGTGAAGAGCAGGCAAACTACAGGCT - 3840  
3841 - GGGTGCAGTCAGGCTTTTTTTTTTTTTTTTTTTTTTAAATAAAGAAAAGCCAGAAATCT - 3900  
3901 - AGAGTTATGTGAGAACTCTAGATTTTTTTCATAGTTAGCAGCTAAAATGGTAAGAGCCAAA - 3960  
3961 - CAAAACCCATCCGTGGGTGGATTGCGCACACATGCCTGCGAATTGCAGTCTCCATGCTG - 4020  
4021 - ATCTCTTGGGCCCTTCTGGGGAGGCAGAGGGAAGGCTCCCTGACTCAGTCACAGGCAATG - 4080  
4081 - GGGAATAGGCAGTGACAGTCATTTTACAGCAGGGTATGTATGTTTAAAGAGTCTAGGCCGG - 4140  
4141 - GGTGTGGTGGCTCACGCCTGTAATTGCAGCACTTTGGGAGGCCGAGGCGGGTGGATCACC - 4200  
4201 - TGAGGGTCAGGAGTTCGAGAACAGCCTGGCCAACATGATGAAATCCCGTCTCTACTAAAA - 4260  
4261 - ATACAAAAATTAGCTGGACATGCTGGCACACGCCTGTAATCCCAGCTACTTGGGAGGCTG - 4320  
4321 - AGGCAGGAGAATGGCTTGAACCCGGGAGGCAGAGGTTGCAGTGAAGTGAAGTGTGCCAC - 4380  
4381 - TACATCCAGCCTGGGTGACAAGAGTGAAACTCTGTCTCAAAAAAAAAAAAAAGAATCTA - 4440  
4441 - GAATCTAAGTCGAGTGTCAATATATCCATGTTTTATTCCCTATTCCCTTTTCCCCTTATGT - 4500  
4501 - ATCCTCTTACTTTAAAGAGGAACCTTAAAAAATCTTAGGGACGACTAGGCAGAGTGGCTC - 4560  
4561 - ACACCTGTAATCCAGCACTTTGGGAGGCCAAGGCAGGAGATTATGAGGTCAGGAGTTC - 4620  
4621 - GAGACCAGCCTGGCCAACATGGTGAAACCCCAAGTTCTACTAAAGATACAAAAAATCAGCC - 4680  
4681 - GGGCGTGGTGGCACGTGCCTATAATCCAGATACTCGGGAGGCTGAGGCAGGAGAATCAC - 4740  
4741 - TTGAACCCGTGAGGCAAAGTTTTTCAGTGAGCTGAGATCATGCCATTGCACTCCACCTGGG - 4800

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fig. 24 (continued, 3/9)

4801 - TGACAGGGTGAGACTCCATCTCAAAAAAGAAAAAGAAAAATCTTAACGTCACATACA - 4860  
 4861 - TGGAAAGATCATCTTTTTTACCCCCACCCCCAACTGAGATGGAGTTTTGCTCTTGTAC - 4920  
 4921 - CCAAGCTGGAGTGCAGTGGCGGATCTAGCTCCCTGCAAGCTCCGCTCCCGGGTTTACA - 4980  
 4981 - CCATTCTCCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCTCCTGCTACCATGCC - 5040  
 5041 - GGCTAATTTTTTTGTATTTTTTTTAGTAGAGACGGGGTTTCATCTGTGTTAGCCAGGATG - 5100  
 5101 - GTTTTGATCTCCTGACCTCGTGATCCGCCGCCCTCAGCCTCCCAAAGTGCTGGGATTACA - 5160  
 5161 - GCGTAAGCCACTGCACCCCGCCTTTTTTTTTTAATTAATTAATTTTTTTAGACAGAGTC - 5220  
 5221 - TCGCTCTGTCCCAAGCTGGAGTGCAGTGGCGGATCTGGGCTCACTGCAACCTCCGCCTC - 5280  
 5281 - CTGGGTTACGGCGATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCTCCTG - 5340  
 5341 - CTACCATGCCCGCTAATTTTTTTGTATTTTTTTTAGTAGAGACGGGGTTTCACTGTGTT - 5400  
 5401 - AGCCAGGATGGTTTTGATCTCCTGACCTCGTGATCCGCCGCCCTCAGCCTCCCAAAGTCC - 5460  
 5461 - GCCTCAGCCTCCCAAAGTGCTGGGATTACAGGCGTAAGCCACTGTACCCTGCCTTTTTTT - 5520  
 5521 - TTTAATTAATTAATTTTTTTAGACAGAGTCTCGCTCTGTCAACCAAGCTGGAGTGCAGTGG - 5580  
 5581 - CGCGATTTGGGCTCACTGCAACCTCCGCTTCTTGGGTTCAAGCGATTTTCTACCTCAGC - 5640  
 5641 - CTCGGAGTAAGTGGGACTACAGGCGGTGCCACCACCAAGCTAATTTTTTTGTGTAT - 5700  
 5701 - GTCTTTAGTAGAGATGGGGTTTACCATGTTAGGATGGTCTCGATCTCTTGACCTCGTGA - 5760  
 5761 - TCCGCTGCCTCGGCCCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCTTGCCCTGGCC - 5820  
 5821 - GAAAGTATCTTCATTTTAAAGTTCAGTGTGTTGGCTACTCTGTTGACAAGAGTTTAGTATT - 5880  
 5881 - TCTCAAGGAGGCTAAGATACTTATCCTTTTGGATCCTACCTCTATCAGGAGGGTGGGC - 5940  
 5941 - CTTCTTGCAATTGAAACAGTATGAAACAGTACGCTGAATTCATAAGTGGGACACCTTT - 6000  
 6001 - CTTCTATTGGTAGAGCAGGCAGTTTTTCTCCTGCCAATGGTGCCCTACTAAGGAGATTT - 6060  
 6061 - CACTAGGGTACAGTCGTTTCAATTTGATAAGCATTTGTTGAGCATATCCTCTGTGATGGTAC - 6120  
 6121 - TATGGACAGTACTGGGGCTATAGTGAGGGCAGGATTGAGTTGGTCCTTATGGCAAGGAAG - 6180  
 6181 - GCAGCTAATCAACAAGCAAAATATAAAGTATGATGGGGAGGGCTGTCTTCAGCACTCATG - 6240  
 6241 - AGTGTGAGCCAGGCCTGGAGGGGACACCTGGAGAAGAGGGTGCATGTCTTTGCTCCTGT - 6300

6301 - GCTTTTCAGGGAAGGAGATCACGTTGCTGATGCAGACATTGAATACTCTGAGTACCCAG - 6360  
 - K E I T L L M Q T L N T L S T P E

6361 - AGGAGAAGCTGGCTGCTCTGTGCAAGAAGTATGCTGAACTGGTCAGTTCCCCCTCCGCG - 6420  
 - E K L A A L C K K Y A E L

6421 - GGCACCTTCCCTGCGTTGGGAAAATCAGCATGCCACCTGGTGTAAGGTTGGGGGTGCAGA - 6480  
 6481 - GTCAAGTAGGTGGCTTAATTCCTGTTAGCTTTTCTCTGAAGTATCTGTTAAATGGGGAA - 6540  
 6541 - TCACTTCCAGCCAGCCTCTTCAGGGCTGTGCAGCAAGAGGAGAACTGCATATTCCTTGA - 6600  
 6601 - AAGAAATTTCTCAAAGAATGATTCCAAGGTGGTAGAGCCCTGTTCTGCGCTGAGTCCA - 6660  
 6661 - AGACACCTTGTGATCTTGATGCTTCTCTCAAATACAGATGCATAGAGCCATTATCACA - 6720  
 6721 - GTTAATAAACTAACACTAGTCACTTGATACTTTTTCTTTTACTCCAGAGCAGTCTTCT - 6780  
 6781 - TGTCACTGCCTCCTCATATCCCCATGACATTGACTTTTAAACAGAACTAGACTAGCTGT - 6840  
 6841 - CTTGTAGGATGCCCCCTTAGCTTTGTCATCTCTGTGGTATCATTTTACTTCTTTACCT - 6900  
 6901 - CCTGGTACATGTAAGTGAAGTAGAAGTATAGCTCTAAAGCTTGATCCAATTCAGCTTCAAC - 6960  
 6961 - TTTTGTACAAGAATTTCTCATAAGTACTTCATGTTCCATCACAATAAATGCAAAGCATGC - 7020  
 7021 - TCTTCCCACTTTGTTGTAACATTGTTCACTGGGTTGGGGGTGGGGCAGCCAGATTCTTCC - 7080  
 7081 - ATCATCAGGTCCCTTGTGAGAATTTGAACTAACAGATTTATCCATTGATGGTCACAGCCT - 7140  
 7141 - GTGTATGTATGTATGTATGTATGTATGTATGTATTTATTTATTTATTTTATTTTGTAGAC - 7200  
 7201 - GGGGTCTTGCTCTGTGCGCCAGGCTGGGGTGCAGTGGCACGATCTCGGCTCGCTGCAAGC - 7260  
 7261 - TCCGCTTCTGGGTTTCATGCCATTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGTCTACAG - 7320  
 7321 - GCGCCGCCACCATGCTAGGCTATTTTTTTTTTTTTTTTTTTTTTTTAGTAGAGACGGGT - 7380  
 7381 - TTACCGTGTAGCCAGGATGGTCTCGATCTCTTGACCTCGTGATCCGCCGCCCTCGGCC - 7440  
 7441 - TCCCAAAGTGCTGGGATTACAGGCTGAGCCACGAGCTGGCCTATTTATTTATTTATT - 7500  
 7501 - CAGAGTCAGAGTCTCGCTCTGTACCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCATT - 7560  
 7561 - GCAACCTCCACCTCCAGGTTCAAGCGAGTCTCCTGCCTCAGCCTCCCGAGTAGCTGGGA - 7620  
 7621 - TTACAGGTGCATGTCAACATGCCTGGCTAAATTTTGTATGTTTTAGTAGAGACAGAGTTT - 7680

FOOTNOTES

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- - - Fig.-24 (continued, 4/9) - - -

7681 - CAGTATGTTGGCCAGGATGGTCTTGATCTCTTGGCCTCGTGATCCGCCCCGTCTCAGCCTC - 7740  
7741 - CCAAAGTGCTGGGATTACAGGTGTGAGCCACTGTGCCTGGCCTCTAAGTATTTATTTTAA - 7800  
7801 - AATTAATTCATTCCACACACATTTATTAATATTTTCTGTAAAGGAACCTTACTCATCTTT - 7860  
7861 - AAAATGGGGAATGTCATACCTGCCTAATGACATTCTTGTAAGGATTAAATAAAAAGGTATA - 7920  
7921 - AGGAAGATAAGCACCCTTTTGGAGTGATCCAGCCAGGGGAAAATTGCTGATGCAAGAGAG - 7980  
7981 - GAAATGAGTTGCTAGAGTGGTGTGTGAGTAGAGGAGGGGAGCTGAGGCCTGCCCAAGAA - 8040  
8041 - GGGGGCTTGGCTGTGGTAACCACATGGCTAGGTCTGTGTGACTGGAGGAGAGGACGGGGC - 8100  
8101 - AGGTGGACTGGTAGATGTGCAGCTTGTGCCCTGATTCTCTAGTTTCTTCTGTGTTTTGA - 8160  
8161 - GATTTGATGAGAACGATGAAATAGTTGTCTGGAAGGAGAGGAGTGTGAATAGCATATGCA - 8220  
8221 - TTGTATTGGGATTGCTGGTCTTCCTGAAATTGGTGGCCATGAATTTAAAGTGAGACTCTT - 8280  
8281 - CAAGTAGGGTTGTTATAGTACTGGTGTAAGCAGGAAGGTGCTTTACTAGGGTTGCAGTA - 8340  
8341 - CTACTGGGGAAGGGCCAAGAGAGTTGAGGGTGTAAGAAATCCAAGCCAGGTAATGTAGTT - 8400  
8401 - ATTTTAAAGGAGAGTGGAAGGATGGTTGAGTCAATGGATTGGAGGTCTATAGGGTAAGA - 8460  
8461 - GACTTCTGAGGATCACAGATACTGATTGGAATGAGCTAAAAAGATAGGTGATGGTAGTC - 8520  
8521 - CTGGACTGGGATGCTGGAAATTGAGATAGTGGGTGTGCTCTCTGGTAGTGACAAATCTAG - 8580  
8581 - ATCTGCGCTGTCCAAGATAAAATCGTCTCTAGCTAATTGACATGTGGCCAGTTTGAATTT - 8640  
8641 - GAACATGCTATAAATGTAAGATACACATCAGCTTTTGAAGACTTAAGCAAAAACAAAGAA - 8700  
8701 - TATAAAACATCTTTTGTGAGAGAGTGTCTCAGTCACCCAGGCTGGAGTGCAGTGGCGTG - 8760  
8761 - ATGTCTTGCTTCCAGGTTCAAACGATTCTCCTGCCTCACAGCCTCCTGGAGTAACTGAGA - 8820  
8821 - TTACAGGCGCATGCCACCAAACTGGCTACTTTTTTGTATTTTTTTTAGTAGAAACGGT - 8880  
8881 - TTCACCATGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTCAAGTGATCTGCCTGCCTCAG - 8940  
8941 - CCTCCCAAAGTGCTGGGATTACAGGCATGAGCCACCCTCCCGCCTCACTTTTTTACAT - 9000  
9001 - TGATTCCGTGTTGAAATTGTAATGTTTTGGATATTAGGTTAAATACATATATTACTAAAA - 9060  
9061 - TTAATTTACCTGTTTTTTACTTTTTTAGTGCGCCAGTAGAATATTTTTTAATTACTTAT - 9120  
9121 - GTGGTTTGCATTATATTCTGTGTACAGGCCTGGATAGGGTCATGGGAGGGGAACTGAG - 9180  
9181 - CTGGGGAAAGGAGTGGGTTTGTGGAAGAGGTGATGGAAGTGTGAGGCCAGGGAGTTAGAAG - 9240  
9241 - GATTATCTGTTGATACTGAAGTGGCCACAAATGAGAAAAGTAATTGTGTTGGGGAGAGCG - 9300  
9301 - CTGATGAACGCAGCGCTAACGTTTTGAAGGAATGCGAGGGAGCGATGGGGGTCTGTCTGT - 9360  
9361 - TAATAGGCACAAGGTACGGTAGCAGGTGGTCTCATCCTCGGGCATGAGTGTCCAGCAAGT - 9420  
9421 - TGGGGAAATGCAACAGCTTGAAGTGGCTCTAGTGGCCCAGAGTCAGAGCTGGAATAGGAA - 9480  
9481 - TTGGCATCTGCTGGCTGTGTGGCCCCCTGCTTGCCCTAGTGAGTTACCATTTCTCTGTCCC - 9540  
9541 - TACGGTGGAGCCTTTGGGGTTATTGTGAGTTCATGGGAGGAGCGTGTAAACACCGGCACA - 9600  
9601 - GCATCAGCCCATGAGAGTGCTCCTGGCCTGAGAGGGTAAGGGTCAGGGCAGCTCAGGAGA - 9660  
9661 - CCCTAGACCTGCATAGTGATCCCCCACCAGGAAGGCCCCACAAGATGCTCACCTGCCCT - 9720

9721 - CCCTATCCCTGTCCCCAGCTGGAGGAGCACCGGAATTCACAGAAGCAGATGAAGCTCCTA - 9780  
- L E E H R N S Q K Q M K L L

9781 - CAGAAAAAGCAGAGCCAGCTGGTGCAAGAGAAGGACCACCTGCGCGGTGAGCACAGCAAG - 9840  
- Q K K Q S Q L V Q E K D H L R G E H S K

9841 - GCCGTCCTGGCCCGCAGCAAGCTTGAGAGCCTATGCCGTGAGCTGCAGCGGCACAACCGC - 9900  
- A V L A R S K L E S L C R E L Q R H N R

9901 - TCCCTCAAGGTAGGCCTGGGCCCCCTGGAACAGGTGACTCTGGTTTCCTTGACTTCCACT - 9960  
- S L K

9961 - TAATGTTTCTTTCATGGGCTTTTCTCTTAAAAAGTAGTGAGGCTAGGGCCAGGCGCAGT - 10020  
10021 - GGCACACATAAGTGATTAAAAATCTTCTGGCCACTAAAAACAGAAATTAATTTTAGTAA - 10080  
10081 - TATACTTAACCAATATCCAAAACATTACAATTTCAACATGAAATCAGTGTAAGGAGCA - 10140  
10141 - AGGCTGGGTGTGGTGGCTCACACCTGTAATCCCAACACTTTGGGAGGCTGAGGTGGATGG - 10200  
10201 - ATCACTTGAGGCCAGGAGTTTGTAGACCAACCTGGTCAACGCAGTGAAACCCCATTTACT - 10260  
10261 - AAAAATACAAAAATTAGCCGAGTGTGCTGGCAAATGCCTATAATCCAGCTACTCAGGTG - 10320

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Fig. 24 (continued, 5/9)

10321 - GCTCAGGCATGAGAATTGCTTGACCTGGGAGGCTGAGGTTGCAGTGAGCCGAGATTGCA - 10380  
 10381 - TCACTGCATTACAGCCTGGGCAACAGAGTGAGACTCAGTGTCACAAAAAAGTA - 10440  
 10441 - GTGCAGGCTTGTGGCATAGAAATACACTTTCTCAATAATGCCTTACGTTAAGAGAGTACT - 10500  
 10501 - GCTTGTAATCATTGTGACATGTATTAGATAAGGTGAAGGATAAAGTACTAAGAGAATCCAT - 10560  
 10561 - AATGCACTGGCGTTAGTATTTCTCAATGAAATGACAGTCCCCTGGTAAGCGGAGGCCTGG - 10620  
 10621 - CTCTGACAAGCAGCTCTTGTCCCAGACGTTGGTCAGTCAGGAACCTGGGTCTTCCCATG - 10680  
 10681 - TTCTGCTGCTTCTATGGTGAGGTGAGTCTGTGGTTACACCAAGTTAAATACAGCCTTTT - 10740  
 10741 - AACTTTCTTTTTTATATGTAAATCTTACATGTAGTTTTTAGAATGAAATTATTATACAT - 10800  
 10801 - GTACCATTTTCATATCCTGTGCCTTTTTTTTCACTTTACATAACATTTTTCCCTATCAGTAT - 10860  
 10861 - GTGTAGGGCTATCTTCTCATTATATGGATATATTATATCAGTGCCCTAGTTAAAGCATTT - 10920  
 10921 - TGGGGGTTGTTTACAATTTTTTCAATTATTACATATAGAACTATAGTGAAAATTCTTGTTAT - 10980  
 10981 - ATTTATCACTGGTCAGTTATATAGAACTTATCTGTAGGATAAGTCATGGAATTGAAATGG - 11040  
 11041 - CTAGGTCACAGTATATGCAGATTTTTTCATTTAATAGATTTTGCTGGATTGCCTTCCAGT - 11100  
 11101 - GAGGGGGCAGTGTGCCTTCCCCATCAAAGTGTTGAGTGCCTAATTCTGCACAACTTTGC - 11160  
 11161 - AAACCCTGGGTGTTACTAAATTTTAACAGCTGGTCTCTGGGGGTACAGAGGGGACAAAT - 11220  
 11221 - GCACATTAATCTGAAATCTGGAAGAATAGGCCTTAGGAGATCCGACTTGCTTCAGAATGG - 11280  
 11281 - CACTTAGCACTTACATGTGTGCATGTGTGCCTGCATTTTTTCTTCTTTTTTTTTTTTG - 11340  
 11341 - GGGACGGAGTCTTGCTCTGTGGCCCATCGCCAGGCTGGAGTGCAGTGGCGCGATCATAG - 11400  
 11401 - CTCACCACAACCTCCGCCTCCCAGGTTCAAATGACTCCTCTGCCTCAGCCTCCCAAGCAG - 11460  
 11461 - CTGGGACCACAGGTGCACACCATCACGCCGCTAATTTTTGTATTTTAGTAGAAAACGGGG - 11520  
 11521 - TTTACCATATTGGCCAGGCTGGTCTCAAACCTGACCTCGTGATCCGCCCACCTCAGC - 11580  
 11581 - CTCCCAAAGTGCTGGGATTACAGGCGTGAGCCACCGCGCCTGCCATGTGCCTGCATTTTT - 11640  
 11641 - CTAGGGGGAGAATCTCACTTGATGTCACCTGATATACAGAGGGGCCATTGGAACCCGCA - 11700  
 11701 - TTGCACAACATCCTGGAGTCTGGCTACTCCACGCTTTGGGAGCAGGGAGGGCTGTTGGCA - 11760  
 11761 - GAGACCATCTGTGGACTAGCTGGGGGACCCTTGTGAGGTAGCAGTGGATGATGGCTCTCG - 11820  
  
 11821 - GGCTGACTTCTTTGCCCAGGAAGAAGGTGTGCAGCGGGCCCCGGGAGGAGGAGGAGAAGCG - 11880  
 - E E G V Q R A R E E E E K R  
 11881 - CAAGGAGGTGACCTCGCACTTCCAGGTGACACTGAATGACATTCAGCTGCAGATGGAACA - 11940  
 - K E V T S H F Q V T L N D I Q L Q M E Q  
 11941 - GCACAATGAGCGCAACTCCAAGCTGCGCCAAGAGAACATGGAGCTGGCTGAGAGGCTCAA - 12000  
 - H N E R N S K L R Q E N M E L A E R L K  
 12001 - GAAGCTGATTGAGCAGTATGAGCTGCGCGAGGAGGTAAGGGTATCACGGACAGCAGTCAT - 12060  
 - K L I E Q Y E L R E E  
  
 12061 - GGCCAGAAATTGTGAGGTTTTGAGTGTGTGCTAGGCACTGGGACAGTACCTTTTCAGGC - 12120  
 12121 - TTCATCCCATTTCTCCCTTTCTTCTCCTCCTCCTCCTTGGGAGGAGAGTAATGTTATTCC - 12180  
 12181 - TCATAGATAAAAAACAGGTGTGGAGAAGAGACTCACTTACAGCCACACAGCCCCAGGTCC - 12240  
 12241 - ACAGTGCCTTGTCCCAAATGACTGGGCCAGGCATCTTTTGAATTAGAACTATCCACATT - 12300  
 12301 - TTAGAATGGAGGTACATGTATGGACTGTGTGTTATATAGCACCTCAGCAGGGCCTTGGG - 12360  
 12361 - GAAGCCAGACACATTAATGTATTTATGCAGTAGAACTTCAAATACTCACCTACATTATG - 12420  
 12421 - GGCTTACAATGATGCAGGTCAAGTCTGGCTGCCAGCTTATGACAATTTCCATTTTCAGAA - 12480  
 12481 - CTTTGTAGAATTTGGAATTGCAGGGGAGGGGTGTACCTGTGATCAGTGATGGACTCCAGA - 12540  
 12541 - GACTGTGTCCTGATTCTTCTGCTCCTGCCACTCAAAGGCAGAAATTTATCAGGCTG - 12600  
 12601 - GGCGTGGTGGCTCATGCCGTGAATCCCAACACTTTGGGAGGCCAAAGCGGGCGGATCACC - 12660  
 12661 - TGAGGTGAGGAGTTCAAGACCAGCCTGGCCAAACATGGTGAAACCCTGTCTCTACTAAAAA - 12720  
 12721 - TACAAAAAATTAGCCAGGTGTGGTGGTGCACGGCTGTAGTCCCAGCTACTCAGGAGCTG - 12780  
 12781 - AGGCAGGAGAATTGCTTGAACCCAGGAGGCAGAGGTTGCAATGAGCCAAGATTGTGCTAC - 12840  
 12841 - TGCACTCTAGCCTGGGTGATATACCGAGACTCCATCTCAAAAAAAAAAAAAAAAAAAGC - 12900  
 12901 - AGGATGTCACTCCCTTTGTCACTGCGTTGGCTGCCACCCAGGCATTGAATCTTTGGAT - 12960

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— Fig. 24 (continued, 6/9) —

12961 - CTTCCCTGCCAGTCACCTGGCTGTTCTGGGCGCGTTCTCATCATGAGAAGGGAGACCTGC - 13020  
13021 - AGCCCCCTTACAGGGCTGGCAGAGGACCTGCTCTGGATTAGGCCCTTTCCTAGCCCCCTGG - 13080  
13081 - GGTGTGGCAGTGGGTGAGACCGGGAAGATCTGCCCTCTTAGGTTTCATAGGCCAAAGTGAT - 13140  
13141 - GATCGTGTGTGCAGGACCTAGAGGGCGCTCCCCTGACCCACCCCTTTCCTTGCCATACTT - 13200  
13201 - CATCCTCTGGGAACAAAGCTGCTTGTTTGGTTTGGAGGGAGTTGGTTTGGTTCTTATCCC - 13260  
13261 - TCAGCGCTGAGACATAGAGGCTTCCTGGGCCACTACAGTGAGACACGAACTTCAAGAATC - 13320  
13321 - TGAATACCCCCGTTTTCTCTCCCCGCCAAGGCAAAAAAGGACTTAGTACTACCTGTGGAG - 13380  
13381 - AAGGAGGTGCAGGACTACCAGGCCCTGCTGCTTGCATTTACAGCCCTCCCCAGACAGAC - 13440  
13441 - ACAGGCACCCTCATCATACCCAACTGGACTTACCTGCTAGGCACCTTCCCTTCCCCATC - 13500  
13501 - CAAAAAATGGAGTTATTTTCCCTTATTTTCAGCAAGTCCAGTTGATTTTACCTTTGAAGT - 13560  
13561 - AGCACCTGAGTCCTTACCTTCTCTCCATCCCTTCTCTCACCTGACACAGGTCTGCAG - 13620  
13621 - CGCTCCTCTAGTAGGCAGGACAGCCATTCCCTGGGGATGCACATGTCTAGTCTTTGCCTA - 13680  
13681 - GATATGGCAAGTCTTTGCCAACTGAGCTAGGCTGTATGTTCTTAGAGGCATTGTTTTTG - 13740  
13741 - CCCATTCTTCCCATTTACAAGAGAATCAGGGACACAGAAGTGAGGGCTTCCAGCCCCATA - 13800  
13801 - GGTGATCAATCCTGGGGTCAGAGATTTGAGTGTGTTTATTGCTTGCCCTTCTTGGGAGCAG - 13860  
13861 - ATTCCATCCATAAACCATGTGCTTACCAAGGTCTGACTCACTGGGAGAGAAACGACGTGA - 13920  
13921 - GGTTGGAAGCTGACCTTCCAGAGACTTGGGGCCCATGTTGTGTGGTACACATGGGAGTC - 13980  
13981 - CATCATATCAGATTGAGATGGGGGCTGGGCAAGTGCCCTGGTCTGTGGCTGTGGGGCT - 14040

14041 - ACCCTGAGAAAGGGAGCGCTGACAAGCCGACTGCTCCCACCATCTTTGTTGCAGCATAT - 14100  
- H I

14101 - CGACAAAGTCTTCAAACACAAGGACCTACAACAGCAGCTGGTGGATGCCAAGCTCCAGCA - 14160  
- D K V F K H K D L Q Q Q L V D A K L Q Q

14161 - GGCCAGGAGATGCTAAAGGAGGCAGAAGAGCGGCACCAGCGGGAGAAGGATTTTGTGAG - 14220  
- A Q E M L K E A E E R H Q R E K D F

14221 - GCTCAGGCCCCAGGGTTGGGGTGGGGGTGTGGGAGGAGACAGGCTGGGCTCTGGCTCAGC - 14280  
14281 - TCATAGCCGGGTATATGGGAGAAGTCTGGCCAGACCAGGCACAGATTCCCTTGAGTACCA - 14340  
14341 - GTCTGAGAGCAGGAAGCCTCAGTGGGTCTGGTGCTTGTGGCTAAAAACCAACATAGCCC - 14400

14401 - CTGGGGGCTTCTGACAGGATCTGGGGTTCTGTCTTGGAATAGCTCCTGAAAGAGGCAGT - 14460  
- L L K E A V

14461 - AGAGTCCCAGAGGATGTGTGAGCTGATGAAGCAGCAAGAGACCCACCTGAAGCAACAGGT - 14520  
- E S Q R M C E L M K Q Q E T H L K Q Q

14521 - GAGAGCATATAACCTGACCCTGTGCCTTCAAGTTTCCCTCACTGGGCCCCATCCTGGGGG - 14580  
14581 - TAGTGAAATGGGACCCTCATTCTAGGACTGGCTGTGTCTGGCTGCTATGACGCCTTGGT - 14640  
14641 - TGAGCTTAGGTGGGCTCAGAGGACTTCATTTGTAGCTCAGAAATGTATTGCTTTTGAGGA - 14700  
14701 - GGTAGGAACAGAAGAGTTTGAAAATCAACATAAAGGCAAAATAAAAGTCACCCTAAGTCT - 14760  
14761 - CCTACTTTCCAGGCTTAGCATTTTGGATTATATCCTTCCAAATATATAGCTTTGCTTTGT - 14820  
14821 - TTTAAGGAAAAATAGTATCTCAATAGAATTACTGGTCAGAGAGTCAAGGACGGGTCTGAG - 14880  
14881 - TGTGTTGACCAGAGTGCCTCCCAGAGAAACCCAGTCTTATCTGTGGGCTGCTTTCTCCCC - 14940

14941 - ACAGCTTGCCCTATACACAGAGAAGTTTGAGGAGTTCCAGAACACACTTTCCAAAAGCAG - 15000  
- L A L Y T E K F E E F Q N T L S K S S



[illegible]

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--- Fig. 24 (continued, 8/9) ---

16982 - CCTGGCCCCATAAAAGGCTCCCATGCTGAGCAGCCCATTGCTGAAGCCAGGATGTTCTGAC - 17041  
17042 - CTGGCTGGCATCTGGCACTTGCAATTTTGGATTTTGTGGGTGAGTTTACGTACATAGGG - 17101  
17102 - CATTTTGCAAGGCCTTGCAAATGCATTTATACCTGTAAGTGTACAGTGGGCTTGCAATTGG - 17161  
17162 - GGATGGGGGTGTGTACAGATGAAGTCAGTGGCTTGTCTGTGAGCTGAAGAGTCTTGAGAG - 17221  
17222 - GGGCTGTCTATCTGTAGCTGCCATCAGTGGCTTGGCAGAAGTGACTTGAGCATTTCTCT - 17281  
17282 - GTCTGATTTGAGGCTCAGACCCCTCCCTGCCCTTCAAGAGCTCAAGACAAGTAATACACCC - 17341  
17342 - AGGTCTTGAAGTGCATTTGTCTTGTGAGCAGGGCTTGGCTTGGTCAGCTCAGGCCCTCCTAG - 17401  
17402 - CTGCTCTGGAGGCTCCTTTGATTCTCTAGACCTGGAAGAGGTGTCCCTAGGCAGAGCCCT - 17461  
17462 - GGCAGGGCGCTCAGAGCTGGGGATTGCTGCCTGGAACAAGGGACCTGGAGAATGTTTTT - 17521  
17522 - GCGTGGGATGATGTGCTGGTCAGGAGCCCCTTGGGCATCGCTTCCCCTGCCCTTTGGTAG - 17581  
17582 - TGCCAGGACCAGGCCAATGATGCTTCTCAGTAGCCTTATCATTACAGGTGCCTCTCTAG - 17641  
17642 - CCTGCACAAATGATTGACAAGAGATCACCCAAAGGATTATTTCTGAAGGTGTTTTTTCT - 17701  
17702 - TTATTTCTTTTTCTTTTTTTTTTTTTTTTTTCTTTTTCTTTTTTTTTTGCACATGACAGTGTT - 17761  
17762 - TGTATTGAGGACCTTCCAAGGAAGAGGGATGCTGTAGCAGTGGTGCCTGGGTGCCTGGCC - 17821  
17822 - TCCAGTGTCCACCTCCTTACCACCCCACTTGGCTCCTTTGCCATCTTGATGCTGAGGT - 17881  
17882 - TTCCTGTTTGGTGAGATCAGGTTGTTTGTGGTAAAAGAAAGGAAAGGGCTTCTGATGGCT - 17941  
17942 - TTGCCACAAGCTTACCTGTGGGTTTCAGTCTGAGAGGGCCACCACAGTCCCATCAGCA - 18001  
18002 - CTGTCTCCATGCGAGCAGTGTCTGGGTCCCATGTCCAGTGCCTCTTTGGCTTCATGGGTT - 18061  
18062 - TTTCTCTTCTCCTGCCCTGCCCCACATGTCATCCTCAAGATTGTCCTGATTCTATT - 18121  
18122 - TCCTGGCACCTCCCTGCCTGTCCTTGGGATTCTACTTCTTCTGTGTGGGAGCCATAG - 18181  
18182 - CTGTTGTCTAACAGGTAAGAAATGAAATTGAACTATTGACTGGGCCCCAGAAATCCATAA - 18241  
18242 - AATGGCTGCAGACAGTTGTTTCTGTGCTCTGTTCTACCCCACTCCAGTACATAACTACT - 18301  
18302 - ATGTACTGTGTAGAGCCATTCTATATGCTGAATGTTCTGCTGTTGCAACTTGCCAGGGT - 18361  
18362 - ATTAGCCAGTGTGTTGTGCAAGCAGTTTCTGGGACAACAGAATGACTCAGACCAAGATG - 18421  
18422 - GATAGGATGGTTAGGGCTTTGCTTCTGTGCTGTTTTCTTTGAAGCTAGTTCATTGTCCTG - 18481  
18482 - CAGGTCCCTTCATCTTCCATACCTAGCCCACTCTTTTAGCCCTTACCTTAAATCTCTCAG - 18541  
18542 - ATAAGTTGGTTTCAAAAGAATGTTAAGTACTGAATCATGTGTGACTGAGACCAGAGATGG - 18601  
18602 - CAAATGAATGGCACACCATTCTCCTTCTCCTGCCCCAGGGCAGGTACCACTGATCTGCA - 18661  
18662 - TCAGAGTTGCCTGCTATTCTCTGGTGTATCCTTCACATCTAGGTGCCCTCAAGCAGCTGT - 18721  
18722 - GTGAGTGTGAGATCTCTGCCATCTCTGGCTGAGATACTGCTGTCTGTGAAGTGTGTTCC - 18781  
18782 - CATGACCTTTTTCTTCCCCTTTGAATCCCTCTGTCTGGAGTAGTCCTTGCCTCTTCTCTGC - 18841  
18842 - TCCAGTAGGGCCTTTTCCCTACCCAGCCCTGTGCCAGGCTAAGCTGGTACAAGAGCTG - 18901  
18902 - CCAACCTCACAGAGTGTGTTGCTAGGCGAGAGGTTGCCGGAAGAGGCAGAGGTATGCAC - 18961  
18962 - CTTCCCCCTTGAAGAGAGGGGAAAGGCCACAGCTACAGTGCCTGCTGCTGATCCAGTGTGGTGGTG - 19021  
19022 - TTCAGCTACCTCTTAATGCCTGTGGAGGACTGGAGCTGCTGGATCCAGTGTGGTGGTG - 19081  
19082 - TAGGAGGCCACAGTGAGCAGGTGGCCCCAGCTGGGTTTCCAGGTGAGGAATGTGGCCCC - 19141  
19142 - CAGGCAAGGTGCAGCCTTTGCTCACAGCTCCATCCATGTCTAGACCTTCAAGGCCAGTCTG - 19201  
19202 - CAGATGAGGTTCCCTACCTTTTTCTTCTCTTATTGACCAATCAACCAATCACTACAGC - 19261  
19262 - TGCTCTGCTTCTGCTTTCCAAAGTAGCCAGGTCTGGGCCAGATGCAGGGGAGGTGCCT - 19321  
19322 - ATCCATGAGTGAAGGCCAGTGTCTTCCCTCACCTGGGTGGGTCCACACTTGTGACCTCAG - 19381  
19382 - TTTTAGGACCAAGATCTGTGTTGGTTTCTTAGATTGCTAGCTTTTCTCCAGGGGACCAC - 19441  
19442 - AGCAGGTGAAGCTCAAGAGCGCATGGCTCTGCTAATAGTAAATTGTTTTTCAGGGCCTGT - 19501  
19502 - CCAGCTGAGAGCTTCATGTCCACCAGATTCTGAGAGGTGTGAGCAGCACTTTTTTTTTTTT - 19561  
19562 - ATTTGTTGTTTGTGTTTCCATGAGGTTATCGGACCATGGGCTGAGCTCAGGCACCTTCTGT - 19621  
19622 - AGGAGACTGTTATTTCTGTAAAGATGGTTATTTAACCTTCTCACCCATCACGGTGGCC - 19681  
19682 - CTGAGGGCTGACCCGGAGGCCAGTGGAGCTGCCTGGTGTCCACGGGGAGGGCCAGGCC - 19741  
19742 - TGCTGAGCTGATTCTCCAGCTGTGCCCAAGCCTTTCGCTTGCACAGCACAGAGGTGG - 19801  
19802 - TCACCCAGGGACAGCCAGGCACCTGCTCCCTTTCGCTTGCCTGGGGGAGGGAGCTGCC - 19861  
19862 - TTCTGTCCCTGTAAGTCTTTTCTTATGGCCAGCCCGCCCACTCAGACTTGTGTAAGC - 19921  
19922 - TGCACTGGCAGCTTTTTTGTCTCCTTTGGGTATTCACAACAGCCAGGGACTTGATTTTGA - 19981  
19982 - TGTATTTTAAACCACATTAAATAAAGAGTCTGTTGCCTTACTTGTTTCTCTCCTGACCTG - 20041  
20042 - TGTATTCCTTTGTTTCTGGATCTGATCCATTAGCCCTTCCATCATCACTGACTTGTTT - 20101  
20102 - AGGTCTGCTGCAGAGCGCCCATGGTGGTTCCCTGGTATCTTACATATTCCACAGTGTCTT - 20161  
20162 - TGAGCAGTCGCCACAGCCTCAGGATGCTGGCATATCACTTGAGCTGCCTGAGTGGAGCC - 20221  
20222 - CTTGGCAAAGTTGGCAAGACCCTTGCTCAGAGAGGATCACACACACACAAAAAGTTTT - 20281

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Fig. 24 (continued, 2/2)

20282 - CCCTGACCTGGGGGCTCACAGGCTAGTGAAGGGAAAAGGTACTTTTAGCTATAGACAGGT - 20341  
20342 - CAATGGTGCTGAGAGCAGAGAGGAGGCCCTGCCCTTCAGCAAGGTGAGGGGGTGATA - 20401  
20402 - CCTGGAATGGCCTTCTGAACCACAGGGCAGGTAGAAGATGAACGTCATTTAGTGATTAAA - 20461  
20462 - TGGTACAGCTGGGAAGCAGGTCCATGGGACTGGGAGAGGGGGTGAGGCTGGGCCCAGAGT - 20521  
20522 - CTGGGTACCAGGTTAAGGAATGTGGGCTAGATCCAGAGGGCAGGGGGGGCAACTGAAGGT - 20581  
20582 - GTTTC AATAGGAAATTGATAGGCTCCAGCAGTAAGGCCAAAAGGCATGGAGCCAGGCATAG - 20641  
20642 - GCCATTTGAGGCCCAGGTTAAGAGGGGTGGACACTCATCTGCTATTTGGGTCTGAGCT - 20701  
20702 - GTGGGTAGGCTCCTATAGCCCTGGCCTGCCCAAGGGAATTCACAGGGGCCTCTAATTGTA - 20761  
20762 - TGCATTCTTTAAGGAGAGCACATTCTCTGTTTCAGTTTTTACACCCCCCATTTACCCACCT - 20821  
20822 - CAAGCATGGGACTCCTATATGGGAGACATGCTGCTGGTGGCCTCACCAGCACCCCTGTTT - 20881  
20882 - TCTCTGGGTCTGGGTTGGTCAGGCACAAAGGATGATATGTGCTGAATGCCAGGAAATG - 20941  
20942 - GCAGAGACAACCCACCTGCCCTTCCCTCCAGGCCTCCACAAATAGATGTGCCACAAATGA - 21001  
21002 - CTGTGACAGTCCCAGCAGAGCCTCTGACCCTTCTAGCTGGGTCTGATACATGTTTTCCA - 21061  
21062 - TGCTGGCCATGTTATTTCTAGTCGCAGATCCTCTGGAGGGTGTGGGGGGGGTGCCGCCCC - 21121  
21122 - AACTCTTGGAGATTCCAAGCAAAGCAGCTCTGAGAATAATGAGGTTTCTGACCCCCCAGT - 21181  
21182 - GAAGCAGCTGAGGATGGGAACCAAGGGGTGCTCCCTCTGTGAGCAGCATTACCACTGTC - 21241  
21242 - TACTCTAGCAGCTCCGGTGGGGAAGGAGAGGGATTCTGTTGTCCCCAGTCTGGGCCCCCT - 21301  
21302 - GGTTATTGAAAAAGTTCGGAATTACTCTTTACCCTTGTGGAGTGTTCTGAGTGTTGGAAG - 21361  
21362 - TACCCAGGAAGAAGCCCTGAGCAGGTGCCCTCAGGAGCAGTGCCCATGGCTCCCCACATC - 21421  
21422 - AGCCAAGAGGCCCAACCCAGGAAGCCACTCCTGCCCGGGGATGGGGAAGGTGGGCTGGG - 21481  
21482 - TGGCTGTGTGCACTGCCCTGGGCCAGCTCACTTGAGCCTGCTGAGCCGCCTGGCCAAACA - 21541  
21542 - TGAGCCTCTCTCCTGTTGTATCAGATGCTGTTCTGGGGACCTGCGCCAGGAGCCTCTGCC - 21601  
21602 - AGGGCTTTAAATAGCTGCCCCCATTGATCTGGCTGCAGGCAGCAGCAGTCACTGGGTC - 21661  
21662 - AGCCTCCATCAGGTGCTCAGGTTTCCCTGAGGACTGGAGTCAGGTGCCAGGGAATCGCGT - 21721  
21722 - GGTCTACCTTATGACCTGGTGTCTCCACACCTGTCTCCTAGGCCTGGGGGGTGGGGAGG - 21781  
21782 - ACTCCTGTCACTTCATCTGCGGCAAAATACAGCCCCCACCCTTACCAGAGAAAAGTGTCT - 21841  
21842 - TGGCATTGTAGAGAGAGGGGTTTTGCCCTCAAAAGACTGTTGCTTACTTTTCAGTAGAATG - 21901  
21902 - GGGAAATGACACTGGTATCTTCCTTAAGGGTTGTTATGGGGATGAAATGTATGTAAAGTGC - 21961  
21962 - TCAATAGGGCACTGGACTCACTCCATTGATGGCTGTCTTTGCTCGAAGTGTCTTCCTGAT - 22021  
22022 - GCTGCTGCTGTTGCTGCTTGTGCTTCTTCTGTGCTTACATTCTCTCTCTCACTCACTC - 22081  
22082 - ACTCTGTCTCTCCTCTCCCCCGCCCCACCCCTTTCTGACAAAGCCACCACATTTTGTA - 22141  
22142 - AGGAAGTGTAGCTTCTCTGAAACTGCCGGGAAAGGGAAAATCTTTTAAATAGACAT - 22201  
22202 - CACACAACCAACAGGGTCCCTAGGTTTCAGGCGGGGAGGTGAGGTCGAGTGAGA - 22255

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